

SEQUENCE LISTING

<110> O'Donnell, Michael E.

Yuzhakov, Alexander

Yurieva, Olga

Jeruzalmi, David

Bruck, Irina

Kuriyan, John

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 60/143,202

<151> 1997-04-08

<150> 08/823,407

<151> 1997-04-08

<150> 09/057,416

<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

<210> 1

<211> 2007

<212> DNA

<213> *Thermus thermophilus*

<400> 1

tccgggggtg gggttccca gtagaccccg gcccctcccg tgagccccctt tacccaggcc 60
gccacccctc ccaggggggc caaggcgtgc aaggagagga acgtccgcac cacgcctat 120
actagccttg tgagcgcctt ctaccgcgc ttccgcggcc tcaccccca ggaggtggtg 180
ggcaggagc acgtgaagga gcccctccctc aaggccatcc gggagggggag gctcgcccg 240
gcctacccctc tctccggggc caggggcgtg ggcaagacca ccacggcgag gctccctcgcc 300
atggcggtgg ggtgccaggg ggaagacccc cttgcgggg tctgcggcca ctgccaggcg 360
gtgcagaggg gcgcccaccc ggacgtggtg gacattgacg ccgcccagcaa caactccgtg 420
gaggacgtgc gggagctgag gaaaaggatc cacccgcggc ccctctctgc ccccaaggaaq 480
gtcttcatcc tggacgaggc ccacatgctc tccaaaagcg cttcaacgc cttccctcaag 540
accctggagg agccccggcc ccacgtcctc ttctgtttcg ccaccaccga gcccggagg 600
atgcggccca ccattcccttc ccgcacccag cacttccgct tccggccgcct cacggaggag 660

gagatcgctt ttaagctccg ggcgcattcgt gaggccgtgg ggcggggaggc ggaggaggag 720
 gcccctccctcc tcctcgcccc cctggcgac gggccctta gggacgcgga aagcctcctg 780
 gagcgcttcc tcctccttgg aaggccccctc acccggaagg aggtggagcg cgcccttaggc 840
 tcccccccaag ggaccgggggt ggcccgagatc gccgcctccc tcgcgaggggg gaaaacggcg 900
 gagggccctgg gcctcgcccc ggcgccttac ggggaagggt acgccccgag gagcctggtc 960
 tcgggccttt tggaggtgtt ccgggaaggc ctctacgcgc cttcgccct cgccggaaacc 1020
 ccccttcccg ccccgccccca ggccctgatc gccgccttgc ccgccttggc cgaggccatg 1080
 gagcgccctcg cccgcgcctc cgacgccttac agcctggagg tggcccttgc ggaggccgg 1140
 aggccctgg ccggcgagggc cctaccccg cccacgggc ctccctcccc agaggtcgcc 1200
 cccaagccgg aaagcccccc gaccccgaa cccccaaggc ccgaggaggc gcccgcactg 1260
 cgggagcggt ggcgggcctt cctcgaggcc ctcaggccca ccctacgggc cttcgtgcgg 1320
 gagggcccgcc cggaggtccg ggaaggccag ctctgcctcg ctcccttggc ggacaaggcc 1380
 ttccactacc gcaaggccctc ggaacagaag gtgaggctcc tcccccttgc ccaggccat 1440
 ttccgggtgg aggaggctgt cctcgcttgc gagggagaaa aaaaaaggct gagcccaagg 1500
 ccccgccccgg ccccacctcc tgaagcgccc gcaccccgcc gcccctccga ggaggaggt 1560
 gagggcgagg aagcgccgg aaggccccgg gaggaggcct tgaggcggtt ggtccgcctc 1620
 ctggggggggc ggggtgcctg ggtgcggcgcc cccaggaccc gggaggcgcc ggaggaggaa 1680
 cccctgagcc aagacgagat aggggggtact ggtatataat gggggcatga cgccgaccac 1740
 cgacactcgga caagagaccg tggacaacat cctcaagcgc ctccgcgtt ttgagggcca 1800
 ggtgcgggggg ctccagaaga tggtgccgc gggccggccc tgcgacgagg tcctcaccca 1860
 gatgaccgccc accaagaagg ccatggaggc ggcggccacc ctgatcctcc acgagttct 1920
 gaacgtctgc gccgcccagg tctccgaggg caaggtgaac cccaagaagc ccgaggagat 1980
 cgcaccatg ctgaagaact tcatcta 2007

<210> 2
 <211> 529
 <212> PRT
 <213> Thermus thermophilus

<400> 2															
Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
1															15
Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
	20														30
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
	35														45
Lys	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly	
	50														60
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
	65														80
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
															95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
290 295 300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
305 310 315 320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
370 375 380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
385 390 395 400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
405 410 415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
420 425 430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
435 440 445

Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
450 455 460

Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Val Glu Ala Glu
465 470 475 480

Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
485 490 495

Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
500 505 510

Ala Pro Glu Glu Glu Pro Leu Ser Gln Asp Glu Ile Gly Gly Thr Gly
515 520 525

Ile

<210> 3
<211> 1590
<212> DNA
<213> Thermus thermophilus

<400> 3
gtgagcgccc tctaccgccc cttccgcccc ctcacccccc aggagggtggt ggggcaggag 60
cacgtgaagg agccccctcct caaggccatc cgggagggga ggctcgcccc ggccttacctc 120
ttctccgggc ccagggcgt gggcaagacc accacggcga ggctcctcgc catggcggtg 180
gggtgccagg gggaaagaccc cccttgcggg gtctgcccc actgccaggc ggtgcagagg 240

ggcgccccacc cggacgtggc ggacattgac gccgccagca acaactccgt ggaggacgtg 300
 cggagctga gggaaaggat ccacctcgcc cccctctctg cccccaggaa ggtcttcata 360
 ctggacgagg cccacatgct ctccaaaagc gccttcaacg ccctcctcaa gaccctggag 420
 gagccccccgc cccacgtcct cttcgcttgc gccaccaccg agcccggagag gatgcccccc 480
 accatcctct cccgcaccca gcacttccgc ttccgccc tcacggagga ggagatcgcc 540
 tttaagctcc ggccatcct ggaggccgtg gggcgggagg cggaggagga ggccctcctc 600
 ctcctcgccc gcctggcga cggggccctt agggacgcgg aaagcctcct ggagcgcttc 660
 ctccctctgg aaggccccct cacccggaag gaggtggagc gcgccttagg ctccccccca 720
 gggaccgggg tggccgagat cgccgcctcc ctcgcgaggg ggaaaacggc ggaggccctg 780
 ggccctcgccc ggccctcta cggggaaaggg tacgccccga ggagcctggc ctcggccctt 840
 ttggaggtgt tccggaaagg cctctacgccc gccttcggcc tcgcggaaac ccccttccc 900
 gccccgcccc aggccctgat cgccgcctatg accgcctgg acgaggccat ggagcgctc 960
 gcccgcgcct ccgacgcctt aagcctggag gtggccctcc tggaggccgg aaggccctg 1020
 gccgcccagg ccctacccca gcccacgggc gctccccc cagaggtcgg ccccaagccg 1080
 gaaagcccccc cgaccccgga acccccaagg cccgaggagg cgccgcacct gcgggagcgg 1140
 tggcgggcct tcctcgaggg cctcaggccc accctacggg cttcgtcgc ggaggccgc 1200
 cggaggtcc gggaaaggca gctctgcctc gctttccccg aggacaaggc cttccactac 1260
 cgcaaggcct cgaaacagaa ggtgaggctc ctccccctgg cccaggccca ttgcgggtg 1320
 gagggaggctg tcctcgctt ggagggagaa aaaaaaagcc tgagcccaag gccccgcccc 1380
 gcccccacctc ctgaagcgcc cgccacccccc ggcctcccg aggaggaggt agaggcggag 1440
 gaagcggcgg aggaggcccc ggaggaggcc ttgaggcggg tggccgcct cctgggggg 1500
 cgggtgctct gggtgccggc gcccaggacc cgggaggcgc cggaggagga acccctgagc 1560
 caagacgaga taggggtac tggtatataa 1590

<210> 4
 <211> 464
 <212> PRT
 <213> Thermus thermophilus

<400> 4															
Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
1															15
Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
	20														30
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
	35														45
Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
	50														60
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
	65														80
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
															85
															90
															95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
180 185 190

Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
290 295 300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
305 310 315 320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
340 345 350

Ser	Pro	Glu	Val	Gly	Pro	Lys	Pro	Glu	Ser	Pro	Pro	Thr	Pro	Glu	Pro
355					360								365		
Pro	Arg	Pro	Glu	Glu	Ala	Pro	Asp	Leu	Arg	Glu	Arg	Trp	Arg	Ala	Phe
370					375								380		
Leu	Glu	Ala	Leu	Arg	Pro	Thr	Leu	Arg	Ala	Phe	Val	Arg	Glu	Ala	Arg
385					390								395		400
Pro	Glu	Val	Arg	Glu	Gly	Gln	Leu	Cys	Leu	Ala	Phe	Pro	Glu	Asp	Lys
							405				410			415	
Ala	Phe	His	Tyr	Arg	Lys	Ala	Ser	Glu	Gln	Lys	Val	Arg	Leu	Leu	Pro
							420				425			430	
Leu	Ala	Gln	Ala	His	Phe	Gly	Val	Glu	Glu	Val	Val	Leu	Val	Leu	Glu
							435				440			445	
Gly	Glu	Lys	Lys	Lys	Pro	Glu	Pro	Lys	Ala	Pro	Pro	Gly	Pro	Thr	Ser
							450				455			460	

<210> 5
<211> 454
<212> PRT
<213> Thermus thermophilus

<400> 5															
Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
1										10					15
Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
					20					25					30
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
													35		40
															45
Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
															50
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
															65
															70
															75
															80
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser

85	90	95
Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu		
100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
240		
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285
Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln		
290	295	300
Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu		
305	310	315
320		
Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala		
325	330	335
Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro		

	340	345	350
Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro			
355	360	365	
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe			
370	375	380	
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg			
385	390	395	400
Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys			
405	410	415	
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro			
420	425	430	
Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu			
435	440	445	
Gly Glu Lys Lys Lys Ala			
450			

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6
cgcaagcttc acgcstacct sttctccggc ac 32

<210> 7
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 7
His Ala Tyr Leu Phe Ser Gly Thr
1 5

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
cgcgaattcg tgctcsggsg gctcctcsag sgtc 34

<210> 9
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 9
Lys Thr Leu Glu Glu Pro Pro Glu His
1 5

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
gcgcggatcc ggagggagaa aaaaaaagcc tcagccca 38

<210> 11
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
gcgcggatcc ggagggagag aagaaaagcc tcagccca 38

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
gaattaaatt cgcgcttcgg gaggtggg 28

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
gcgcgaattc gcgcattcggg aggtggg 27

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
gcgcgaattc gggcgcttca ggaggtggg 29

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gtggtgata tggtgagcgc cctctaccgc c 31

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
gtggtgttcg acccaggagg gccacacctccaa g 31

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (2)
<223> X is any aa at position 2

<220>
<221> PEPTIDE
<222> (3)
<223> X is any aa at position 3

<220>
<221> PEPTIDE
<222> (5)
<223> X is any aa at position 5

<400> 17
Gly Xaa Xaa Gly Xaa Gly Lys Thr
1 5

<210> 18
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 18

Lys Pro Asp Pro Lys Ala Pro Pro Gly Pro Thr Ser
1 5 10

<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val
180

<210> 20
 <211> 180
 <212> PRT
 <213> Bacillus subtilis

<400> 20
 Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
 1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
 20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
 35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
 50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
 65 70 75 80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
 85 90 95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
 100 105 110

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
 115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
 130 135 140

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
 145 150 155 160

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
 165 170 175

Arg Ile Thr Ser
 180

<210> 21
 <211> 294
 <212> PRT

<213> Escherichia coli

<400> 21

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn
180 185 190

Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg
195 200 205

Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met
225 230 235 240

Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met
245 250 255

Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala
260 265 270

Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu
275 280 285

Leu His Arg Ile Ala Met
290

<210> 22

<211> 294

<212> PRT

<213> Haemophilus influenzae

<400> 22

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
20 25 30

Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
50 55 60

Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
65 70 75 80

Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
100 105 110

Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
225 . 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
275 280 285

Leu His Gln Ile Ala Leu
290

<210> 23

<211> 294

<212> PRT

<213> *Bacillus subtilis* .

<400> 23

Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65

70

75

80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
85 90 95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
100 105 110

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145 150 155 160

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
165 170 175

Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp
180 185 190

Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser
195 200 205

Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala
210 215 220

Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile
225 230 235 240

Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu
245 250 255

His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu
260 265 270

Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr
275 280 285

Phe Arg Asp Met Leu Leu
290

<210> 24

<211> 300

<212> PRT

<213> Caulobacter crescentus

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
1 5 10 15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
20 25 30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
35 40 45

Val Gly Lys Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
50 55 60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
65 70 75 80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
85 90 95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
100 105 110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile
115 120 125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140

Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
85 90 95

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
100 105 110

His Pro Phe Thr Phe Lys Lys Val Tyr Ile Leu Asp Glu Ala His
115 120 125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
130 135 140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Glu Phe Asn Lys
145 150 155 160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
165 170 175

Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
180 185 190

Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
195 200 205

Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
210 215 220

Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
225 230 235 240

Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
245 250 255

Tyr Gln Glu Ile
260

<210> 26

<211> 289

<212> PRT

<213> Thermus thermophilus

<400> 26

Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
1 5 10 15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
85 90 95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu

100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285

Tyr

<210> 27
<211> 94
<212> DNA
<213> Thermus thermophilus

<400> 27
gccggaggga gaaaaaaaaa gccgagccca aggccccgcc cggccccacc ccgaagcgcc 60
cgcaccccccgg ggcgggggggg ggaggaggag aggc 94

<210> 28
<211> 11
<212> PRT
<213> Thermus thermophilus

<400> 28
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (6)
<223> N at position 6 is either G or C

<220>
<221> unsure
<222> (12)
<223> N at position 12 is either G or C

<220>
<221> unsure
<222> (21)
<223> N at position 21 is either G or C

<400> 29
cacgcntacc tnttctccgg nac 23

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure

<222> (7)
<223> N at position 7 is either G or C

<220>
<221> unsure
<222> (10)
<223> N at position 10 is either G or C

<220>
<221> unsure
<222> (19)
<223> N at position 19 is either G or C

<220>
<221> unsure
<222> (22)
<223> N at position 22 is either G or C

<400> 30
gtgctcnggn ggctcctcnt cngtc

25

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa

33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggsctstcs gagcagaag

29

<210> 33
<211> 34

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
gcgggatcct caacgaggac ctctccatct tcaa 34

<210> 34
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 34
gcgggatcct tgtcgtsag sgtsagsgcg tcgta 35

<210> 35
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 35
ggaaaggacc agcgctact cccccctgctc ctaggtgtg 39

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 36
gtgtggatcc ttcttcttsc ccatsgc 27

<210> 37
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 37
caccgattcc agtggtgccct aggtgtg 27

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 38
caacacctgg tggccagga gcctgtgctt 30

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 39
ccagaatcg ctgctggtcg tag 23

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40
agcacccctgg aggagcttc 19

<210> 41
<211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
catgtcgtac tgggtgtac

19

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (7)
<223> N at position 7 is A, C, G, or T

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (13)
<223> N at position 13 is A, C, G, or T

<220>
<221> unsure
<222> (14)
<223> N at position 14 is A, C, G, or T

<400> 42
gtsgtsnnsg acnnsgagac sacsggg

27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer
<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (9)
<223> N at position 9 is A, C, G, or T

.
<220>
<221> unsure
<222> (17)
<223> N at position 17 is A, C, G, or T

<220>
<221> unsure
<222> (18)
<223> N at position 18 is A, C, G, or T

<400> 43
gaasccsnng tcgaasnngg cggttgtg

27

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
cggggatcca cctcaatcac ctctgtgg

27

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 45
cggggatccg ccacacctgcg gctccgggtg

30

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
gcgtctaga cgagttcca aagcgtgcgg t 31

<210> 47
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
cggtctaga tcacctgtat ccaga 25

<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 48
gcggcgata tggtggtggt cctggacctg gag 33

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
cggtctaga tcacctgtat ccaga 25

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 50
gtscctsgtsa agacscactt 20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 51
sagsagsgcg ttgaasgtgt g 21

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 52
ctcgttggtg aaagttccg tg 22

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 53
ctcgttggtg aaagttccg tg 22

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 54
tctggcaaca cgttctggag cacatcc 27

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
tgctggcggtt catcttcagg atg 23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
catcctgaag atgaacgcc a 23

<210> 57
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
aggtttatcca caggggtcat gtgca 25

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gtgtgtcata tgaacataac gttcccaa 29

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
gcgcgaattc tcccttgtgg aaggcttag 29

<210> 60
<211> 13
<212> PRT
<213> Thermus thermophilus

<400> 60
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Thermus thermophilus

<400> 61
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
1 5 10

<210> 62
<211> 8

<212> PRT
<213> Thermus thermophilus

<400> 62
Phe Phe Ile Glu Ile Gln Asn His
1 5

<210> 63
<211> 8
<212> PRT
<213> Thermus thermophilus

<400> 63
Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

<210> 64
<211> 6
<212> PRT
<213> Thermus thermophilus

<400> 64
Ala Met Gly Lys Lys Lys
1 5

<210> 65
<211> 9
<212> PRT
<213> Thermus thermophilus

<400> 65
Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

<210> 66
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE

```
<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 66
Val Val Xaa Asp Xaa Glu Thr Thr Gly
    1           5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (4)
<223> Xaa at position 4 is undefined

<220>
<221> PEPTIDE
<222> (7)
<223> Xaa at position 7 is undefined

<400> 67
His Asn Ala Xaa Phe Asp Xaa Gly Phe
    1           5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (3)
<223> Xaa at position 3 is undefined
```

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 68
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 69
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 69
Val Leu Val Lys Thr His Leu
1 5

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 70
His Arg Ala Leu Tyr Asp
1 5

<210> 71
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 71
His Thr Phe Asn Ala Leu Leu
1 5

<210> 72
<211> 34
<212> PRT
<213> Escherichia coli

<400> 72
Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
20 25 30

Val Val

<210> 73
<211> 34
<212> PRT
<213> Vibrio cholerae

<400> 73
Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
20 25 30

Val Val

<210> 74
<211> 34
<212> PRT
<213> Haemophilus influenzae

<400> 74
Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu
1 5 10 15

Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
20 25 30

Leu Val

<210> 75
<211> 34
<212> PRT
<213> Rickettsia prowazekii

<400> 75
Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
1 5 10 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
20 25 30

Ile Val

<210> 76
<211> 34
<212> PRT
<213> Helicobacter pylori

<400> 76
Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
20 25 30

Ile Ile

<210> 77
<211> 34
<212> PRT
<213> Synechocystis sp.

<400> 77
Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
20 25 30

Ile Val

<210> 78
<211> 34
<212> PRT
<213> Mycobacterium tuberculosis

<400> 78
Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79
<211> 46
<212> PRT
<213> Escherichia coli

<400> 79
Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80
<211> 46
<212> PRT
<213> Vibrio cholerae

<400> 80
Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81
<211> 46
<212> PRT
<213> Haemophilus influenzae

<400> 81
Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 82
<211> 46
<212> PRT
<213> Rickettsia prowazekii

<400> 82
Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
35 40 45

<210> 83
<211> 45
<212> PRT
<213> Helicobacter pylori

<400> 83
Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
35 40 45

<210> 84
<211> 46
<212> PRT
<213> Synechocystis sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15

Leu Pro Asp Asp Val Lys Thr His Lys Leu Leu Glu Ala Gly Asp
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
35 40 45

<210> 85

<211> 46

<212> PRT

<213> Mycobacterium tuberculosis

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
1 5 10 15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

atgggccggg agctccgctt cgcccacctc caccagcaca cccagttctc ctcctggac 60
ggggcgccga agctttccga cctcctcaag tgggtcaagg agacgacccc cgaggacccc 120
gccttggcca tgaccgacca cggcaacctc ttccggggccg tggagttcta caagaaggcc 180
accgaaatgg gcatcaagcc catcctgggc tacgaggcct acgtggcggc ggaaagccgc 240
tttgaccgca agcggggaaa gggcttagac ggggctact ttcacctcac ctcctcgcc 300
aaggacttca cgggttacca gaacctggtg cgcctggcga gccgggctta cctggagggg 360
ttttacgaaa agccccggat tgaccgggag atcctgcgcg agcacgccc gggcctcata 420
gccctctcgg ggtgcctcgg ggcggagatc ccccaagtca tcctccagga ccgtctggac 480
ctggccgagg cccggctcaa cgagtacctc tccatttca aggaccgctt cttcatcgag 540
atccagaacc acggcctccc cgagcagaaa aaggtaacg aggtcctcaa ggagttcgcc 600
cgaaagtacg gcctggggat ggtggccacc aacgacggcc attacgtgag gaaggaggac 660
gccccggccc acgaggtcct cctcgccatc cagtccaaga gcaccctgga cgaccccggg 720
cgctggcgct tccccctgcga cgagttctac gtgaagaccc ccgaggagat gcgggcatg 780
ttccccgagg aggagtgggg ggacgagccc tttgacaaca ccgtggagat cgcccgatg 840

tgcaacgtgg agctgcccatt cggggacaag atggtctacc gaatcccccg cttccccctc 900
cccgaggggc ggaccgaggc ccagtacccctc atggagctca ccttcaggg gctccctccgc 960
cgctacccgg accggatcac cgagggcttc taccgggagg tcttccgcct tttggggaaag 1020
cttccccccc acggggacgg ggaggccttg gccgaggcct tggcccaggt ggagcgggag 1080
gcttggaga ggctcatgaa gagcctcccc ccttggccg gggtaagga gtggacggcg 1140
gaggccattt tccaccggc ctttacgag ctttccgtga tagagcgcatt ggggttccc 1200
ggctacttcc tcatacgcca ggactacatc aactgggccc ggagaaaacgg cgtccctcg 1260
ggggccggca gggggagcgc cgccgggagc ctgggtggcct acgcccgtgg gatcaccaac 1320
attgacccccc tccgcttcgg cttctctttt gagcgttcc tgaacccgga gagggtctcc 1380
atgccccaca ttgacacgga cttctccgac cgggagcggg accgggtgat ccagtagtgc 1440
cgggagcgc acggcgagga caaggtggcc cagatcgca ccctggaaag cctccctcc 1500
aaggccgccc tcaaggacgt gggccgggtc tacggcatcc cccacaagaa ggcggaggaa 1560
ttggccaagc tcataccggc gcaagttcggg aagcccaagc ccctgcagga ggcacatccag 1620
gtgggtccgg agcttagggc ggagatggag aaggacccca aggtgcggga ggtcctcgag 1680
gtggccatgc gcctggaggg cctgaaccgc cacgcctccg tccacgcccgc cgggggtgg 1740
atcgccgccc agcccccac ggacctcgtc cccctcatgc gcgaccagga agggcggccc 1800
gtcaccctgt acgacatggg ggcgggtggag gccttggggc ttttgaagat ggacttttg 1860
ggcctccgca ccctcacctt cttggacgag gtcaagcgc tctgtcaaggc gtcccagggg 1920
gtggagctgg actacgatgc cttcccccgt gacgacccca agacccctgc cctccctctcc 1980
cggggggaga ccaagggggt ctccagctg gagtcggggg ggtgaccgc cacgctccgc 2040
ggcctcaagc cgccggcgtt tgaggacctg atcgccatcc tctccctcta ccggccggg 2100
cccatggagc acatccccac ctacatccgc cgccaccacg ggctggagcc cgtgagctac 2160
agcagtttc cccacgcccga gaagtaccta aagcccatcc tggacgagac ctacggcatc 2220
cccgtctacc aggagcagat catgcagatc gcctcgccg tggcggggta ctccctggc 2280
gaggcggacc tcctgcggcgtt gtcacatggc aagaagaagg tggaggagat gaagtcccac 2340
cgggagcgtc tcgtccaggg gccaaggaa agggcgtgc ccgaggagga ggcacccgc 2400
ctctttgaca tgctggaggc cttcgccaaac tacggcttca acaaattccca cgctgccgc 2460
tacagcctcc tctcctacca gaccgcctac gtgaaggccc actacccgtt ggagttcatg 2520
gcccgcctcc tctccgtggc gccgcacgc tccgacaagg tggccgagta catccgcac 2580
gccccggcca tgggcataga ggtccttccc ccggacgtca accgctccgg gtttgacttc 2640
ctggtccagg gccggcagat cttttcggc ctctccgcgg tgaagaacgt gggcgaggcg 2700
gcggcggagg ccattctccg ggagcggggag cggggcggcc cctaccggag cctccgcac 2760
ttcctcaagc ggctggacga gaaggtgctc aacaagcga ccctggagtc cctcatcaag 2820
gcgggcggccc tggacggctt cggggaaagg ggcggctcc tcgcctccct ggaagggctc 2880
ctcaagtggg cggccgagaa cccggagaag gcccgtcgg gcatgtatggg cctcttcagc 2940
gaagtggagg agccgcctt gggcgaggcc gccccctgg acgagatcac ccggctccgc 3000
tacgagaagg agggccctggg gatctacgtc tccggccacc ccattttgcg gtaccccg 3060
ctccggaga cggccacccgt caccctggag gagcttcccc acctggccc ggcacccgc 3120
ccccggctca gggctccctt tgccggatgt gtggaggagg tggcgcgca gcccacaaag 3180
agccggcggga tggatggcccg ctccgtccctc tccgacgaga cggggccgt tgaggcgg 3240
gcattccggcc gggccctacga ccaggtctcc ccgaggctca aggaggacac ccccggtctc 3300
gtcctcgccg aggtggagcg ggaggagggg ggcgtgcggg tgctggccca ggcgtttgg 3360
acctacgagg agctggagca ggtccccgg gcccctcgagg tggaggtgga ggcctccctc 3420
ctggacgacc ggggggtggc ccacctgaaa agcctccctgg acgagcaccgc ggggaccctc 3480
cccctgtacg tccgggtcca gggcgccttc ggcgaggccc tcctcgccct gaggagggtg 3540
cggggtgggg aggaggctgtt aggcggccgc gtgggtccgg gcctacctcc tgcccgaccg 3600
ggaggtcctt ctccaggccg gccaaggcggg ggaggcccag gaggcgggtgc ccttctaggg 3660
ggtggccgt gagacccatgc gccatcgatc tcggccgggg caaggaggcc tggcccgac 3720

ccctttgg

3729

<210> 87
<211> 1245
<212> PRT
<213> Thermus thermophilus

<400> 87
Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
165 170 175

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
180 185 190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His
 210 215 220

Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly
 225 230 235 240

Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu
 245 250 255

Met Arg Ala Met Phe Pro Glu Glu Glu Val Gly Gly Arg Ser Pro Leu
 260 265 270

Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly
 275 280 285

Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg
 290 295 300

Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg
 305 310 315 320

Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg
 325 330 335

Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu
 340 345 350

Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser
 355 360 365

Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe
 370 375 380

His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro
 385 390 395 400

Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys
 405 410 415

Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val
 420 425 430

Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu
 435 440 445

Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile
 450 455 460

Asp Thr Asp Phe Ser Asp Arg Glu Arg Asp Arg Val Ile Gln Tyr Val
465 470 475 480

Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly
485 490 495

Ser Leu Ala Ser Lys Ala Ala Leu Lys Glu Val Ala Arg Val Tyr Gly
500 505 510

Ile Pro Arg Lys Lys Ala Glu Glu Leu Ala Lys Leu Ile Pro Val Gln
515 520 525

Phe Gly Lys Pro Lys Pro Leu Gln Glu Ala Ile Gln Val Val Pro Glu
530 535 540

Leu Arg Ala Glu Met Glu Lys Asp Pro Lys Val Arg Glu Val Leu Glu
545 550 555 560

Val Ala Met Arg Leu Glu Gly Leu Asn Arg His Ala Ser Val His Ala
565 570 575

Gly Arg Gly Gly Val Phe Ser Glu Pro Leu Thr Asp Leu Val Pro Leu
580 585 590

Cys Ala Thr Arg Lys Gly Gly Pro Tyr Thr Gln Tyr Asp Met Gly Ala
595 600 605

Val Glu Ala Leu Gly Leu Leu Lys Met Asp Phe Leu Gly Leu Arg Thr
610 615 620

Leu Thr Phe Leu Asp Glu Val Lys Arg Ile Val Lys Ala Ser Gln Gly
625 630 635 640

Val Glu Leu Asp Tyr Asp Ala Leu Pro Leu Asp Asp Pro Lys Thr Phe
645 650 655

Ala Leu Leu Ser Arg Gly Glu Thr Lys Gly Val Phe Gln Leu Glu Ser
660 665 670

Gly Gly Met Thr Ala Thr Leu Arg Gly Leu Lys Pro Arg Arg Phe Glu
675 680 685

Asp Leu Ile Ala Ile Leu Ser Leu Tyr Arg Pro Gly Pro Met Glu His
690 695 700

Ile Pro Thr Tyr Ile Arg Arg His His Gly Leu Glu Pro Val Ser Tyr
705 710 715 720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu
725 730 735

Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser
740 745 750

Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser
755 760 765

Met Gly Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe
770 775 780

Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Ala Asn Arg
785 790 795 800

Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser
805 810 815

His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys
820 825 830

Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg
835 840 845

His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met
850 855 860

Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe
865 870 875 880

Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn
885 890 895

Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly
900 905 910

Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys
915 920 925

Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu
930 935 940

Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu
945 950 955 960

Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met
965 970 975

Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro
980 985 990

Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile
995 1000 1005

Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr
1010 1015 1020

Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro
1025 1030 1035 1040

Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg
1045 1050 1055

Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp
1060 1065 1070

Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln
1075 1080 1085

Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu
1090 1095 1100

Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp
1105 1110 1115 1120

Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val
1125 1130 1135

Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu
1140 1145 1150

Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly
1155 1160 1165

Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu
1170 1175 1180

Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu
1185 1190 1195 1200

Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg
1205 1210 1215

Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala
1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
1235 1240 1245

<210> 88
<211> 198
<212> PRT
<213> Thermus thermophilus

<400> 88
Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
1 5 10 15

Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
20 25 30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
35 40 45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Arg Arg
50 55 60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
65 70 75 80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Ala Pro
85 90 95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
100 105 110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
115 120 125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
130 135 140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu
145 150 155 160

Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
165 170 175

Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
180 185 190

Tyr Met Leu Thr Ser Gly
195

<210> 89
 <211> 182
 <212> PRT
 <213> Deinococcus radiodurans

<220>
 <221> PEPTIDE
 <222> (79)
 <223> X at position 79 is undefined

<400> 89
 Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
 1 5 10 15

Ser	Pro	Ala	Ser	Ala	Ala	Ile	Val	Glu	Ile	Gly	Ala	Val	Arg	Ile	Val
							20		25						30

Gly	Gly	Gln	Ile	Asp	Glu	Thr	Leu	Lys	Phe	Glu	Thr	Leu	Val	Arg	Pro
							35		40						45

Thr	Arg	Pro	Asp	Gly	Ser	Met	Leu	Ser	Ile	Pro	Trp	Gln	Ala	Gln	Arg
							50		55						60

Val	His	Gly	Ile	Ser	Asp	Glu	Met	Val	Arg	Arg	Ala	Pro	Ala	Xaa	Lys
							65		70						80

Asp	Val	Leu	Pro	Asp	Phe	Phe	Asp	Phe	Val	Asp	Gly	Ser	Ala	Val	Val
							85		90						95

Ala	His	Asn	Val	Ser	Phe	Asp	Gly	Gly	Phe	Met	Arg	Ala	Gly	Ala	Glu
							100		105						110

Arg	Leu	Gly	Leu	Ser	Trp	Ala	Pro	Glu	Arg	Glu	Leu	Cys	Thr	Met	Gln
							115		120						125

Leu	Ser	Arg	Arg	Ala	Phe	Pro	Arg	Glu	Arg	Thr	His	Asn	Leu	Thr	Val
							130		135						140

Leu	Ala	Glu	Arg	Leu	Gly	Leu	Glu	Phe	Ala	Pro	Gly	Gly	Arg	His	Arg
							145		150						160

Ser	Tyr	Gly	Asp	Val	Gln	Val	Thr	Ala	Gln	Ala	Tyr	Leu	Arg	Leu	Leu
							165		170						175

Glu	Leu	Leu	Gly	Glu	Arg										
						180									

<210> 90
 <211> 201
 <212> PRT
 <213> Bacillus subtilis

<400> 90
 His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
 1 5 10 15

Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
 20 25 30

Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
 35 40 45

Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
 50 55 60

Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
 65 70 75 80

Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
 85 90 95

Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
 100 105 110

Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
 115 120 125

Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
 130 135 140

Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
 145 150 155 160

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 165 170 175

His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
 180 185 190

Lys Met Leu Lys Asp Ala Ala Glu Lys
 195 200

<210> 91
<211> 188
<212> PRT
<213> Haemophilus influenzae

<220>
<221> PEPTIDE
<222> (47)
<223> X at position 47 is undefined

<220>
<221> PEPTIDE
<222> (57)
<223> X at position 57 is undefined

<400> 91
Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
1 5 10 15

Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
20 25 30

Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
35 40 45

Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
50 55 60

His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
65 70 75 80

Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
85 90 95

His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
100 105 110

Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
115 120 125

Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
130 135 140

Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
145 150 155 160

Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
165 170 175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
180 185

<210> 92
<211> 189
<212> PRT
<213> Escherichia coli

<400> 92
Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
1 5 10 15

Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
 20 25 30

Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
 35 40 45

His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
50 55 60

His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
65 70 75 80

Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
85 90 95

His	Asn	Ala	Ala	Phe	Asp	Ile	Gly	Phe	Met	Asp	Tyr	Glu	Phe	Ser	Leu
				100				105				110			

Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
 115 120 125

Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
130 135 140

Asp	Ala	Leu	Cys	Ala	Arg	Tyr	Glu	Ile	Asp	Asn	Ser	Lys	Arg	Thr	Leu
145					150					155					160

His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
165 170 175

Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
180 185

<210> 93
<211> 201
<212> PRT
<213> Helicobacter pylori

<400> 93

Asn	Leu	Glu	Tyr	Leu	Lys	Ala	Cys	Gly	Leu	Asn	Phe	Ile	Glu	Thr	Ser
1		5							10						15
Glu	Asn	Leu	Ile	Thr	Leu	Lys	Asn	Leu	Lys	Thr	Pro	Leu	Lys	Asp	Glu
	20							25							30
Val	Phe	Ser	Phe	Ile	Asp	Leu	Glu	Thr	Thr	Gly	Ser	Cys	Pro	Ile	Lys
	35							40							45
His	Glu	Ile	Leu	Glu	Ile	Gly	Ala	Val	Gln	Val	Lys	Gly	Gly	Glu	Ile
	50							55							60
Ile	Asn	Arg	Phe	Glu	Thr	Leu	Val	Lys	Val	Lys	Ser	Val	Pro	Asp	Tyr
	65						70			75					80
Ile	Ala	Glu	Leu	Thr	Gly	Ile	Thr	Tyr	Glu	Asp	Thr	Leu	Asn	Ala	Pro
		85						90							95
Ser	Ala	His	Glu	Ala	Leu	Gln	Glu	Leu	Arg	Leu	Phe	Leu	Gly	Asn	Ser
		100						105							110
Val	Phe	Val	Ala	His	Asn	Ala	Asn	Phe	Asp	Tyr	Asn	Phe	Leu	Gly	Arg
		115						120							125
Tyr	Phe	Val	Glu	Lys	Leu	His	Cys	Pro	Leu	Leu	Asn	Leu	Lys	Leu	Cys
		130				135									140
Thr	Leu	Asp	Leu	Ser	Lys	Arg	Ala	Ile	Leu	Ser	Met	Arg	Tyr	Ser	Leu
	145							150		155					160
Ser	Phe	Leu	Lys	Glu	Leu	Leu	Gly	Phe	Gly	Ile	Glu	Val	Ser	His	Arg
			165						170						175
Ala	Tyr	Ala	Asp	Ala	Leu	Ala	Ser	Tyr	Lys	Leu	Phe	Glu	Ile	Cys	Leu
			180					185							190
Leu	Asn	Leu	Pro	Ser	Tyr	Ile	Lys	Thr							
			195					200							

<210> 94
<211> 630

<212> DNA

<213> Thermus thermophilus

<400> 94

atgggtggagc ggggtggtgcg gacccttctg gacgggaggt tcctcctgga ggagggggtg 60
gggctttggg agtggcgcta cccctttccc ctggaggggg aggcggtggt ggtcctggac 120
ctggagacca cggggcgttgc cggcctggac gaggtgattg aggtggggct cctccgcctg 180
gagggggggg ggcgcctccc cttccagagc ctcgtccggc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcaccgg catccccgg gaggccctgg aggaggcccc ctccctggag 300
gaggttctgg agaaggccta cccctccgc ggcgacgcca ctttgggtgat ccacaacgcc 360
gccttgacc tgggcttcct ccgccccggcc ttggagggcc tgggctaccg cctggaaaac 420
cccggtgtgg actccctgcg cttggccaga cggggcttac caggccttag ggcgtacggc 480
ctggacgccc tctccgaggt cctggagctt ccccgaaagga cctgccaccg ggccctcgag 540
gacgtggagc gcaccctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttggaaact cgggaggtag 630

<210> 95

<211> 210

<212> PRT

<213> Thermus thermophilus

<400> 95

Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
1 5 10 15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
20 25 30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
35 40 45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
50 55 60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
65 70 75 80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
85 90 95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
100 105 110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
115 120 125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp

130	135	140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly		
145	150	155
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His		
165	170	175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val		
180	185	190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly		
195	200	205
Arg Glx		
210		
<210> 96		
<211> 461		
<212> PRT		
<213> Pseudomonas marcesans		
<400> 96		
Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn		
1	5	10
		15
Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser		
20	25	30
Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser		
35	40	45
Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala		
50	55	60
Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala		
65	70	75
		80
Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro		
85	90	95
Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu		
100	105	110
Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe		
115	120	125

Asn	Arg	Phe	Val	Val	Gly	Pro	Asn	Ser	Arg	Met	Ala	His	Ala	Ala	Ala
130							135				140				
Met	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe	Ile
145								150			155			160	
Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	Gly
								165		170			175		
His	Tyr	Arg	Leu	Glu	Ile	Asp	Pro	Gly	Ala	Lys	Val	Ser	Tyr	Val	Ser
								180		185			190		
Thr	Glu	Thr	Phe	Thr	Asn	Asp	Leu	Ile	Leu	Ala	Ile	Arg	Gln	Asp	Arg
								195		200			205		
Met	Gln	Ala	Phe	Arg	Asp	Arg	Tyr	Arg	Ala	Ala	Asp	Leu	Ile	Leu	Val
								210		215			220		
Asp	Asp	Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	Phe
								225		230			235		240
Phe	His	Thr	Phe	Asn	Ala	Leu	His	Asp	Ala	Gly	Ser	Gln	Ile	Val	Leu
								245		250			255		
Ala	Ser	Asp	Arg	Pro	Pro	Ser	Gln	Ile	Pro	Arg	Leu	Gln	Glu	Arg	Leu
								260		265			270		
Met	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Val	Gln	Ala	Pro	Asp
								275		280			285		
Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	His	Glu	Arg
								290		295			300		
Val	Gly	Leu	Pro	Arg	Asp	Leu	Ile	Gln	Phe	Ile	Ala	Gly	Arg	Phe	Thr
								305		310			315		320
Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Thr	Arg	Ala	Ile	Ala	Phe
								325		330			335		
Ala	Ser	Ile	Thr	Gly	Leu	Pro	Met	Thr	Val	Asp	Ser	Ile	Ala	Pro	Met
								340		345			350		
Leu	Asp	Pro	Asn	Gly	Gln	Gly	Val	Glu	Val	Thr	Pro	Lys	Gln	Val	Leu
								355		360			365		
Asp	Lys	Val	Ala	Glu	Val	Phe	Lys	Val	Thr	Pro	Asp	Glu	Met	Arg	Ser
								370		375			380		

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
385 390 395 400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr
405 410 415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
420 425 430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
435 440 445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
450 455 460

<210> 97

<211> 447

<212> PRT

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly
35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
130 135 140

Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile
145 150 155 160

Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Tyr Val
165 170 175

Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp
180 185 190

Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu
195 200 205

Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu
210 215 220

Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val
225 230 235 240

Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg
245 250 255

Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro
260 265 270

Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp
275 280 285

Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr
290 295 300

Thr Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Ala Ile Ala
305 310 315 320

Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro
325 330 335

Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile
340 345 350

Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu
355 360 365

Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met
370 375 380

Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu
385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
 405 410 415

 Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
 420 425 430

 Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
 435 440 445

 <210> 98
 <211> 446
 <212> PRT
 <213> Bacillus subtilis

 <400> 98
 Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
 1 5 10 15

 Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
 20 25 30

 Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
 35 40 45

 Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
 50 55 60

 Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
 65 70 75 80

 Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
 85 90 95

 Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
 100 105 110

 Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
 115 120 125

 Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
 130 135 140

 Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
 145 150 155 160

 Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys

165	170	175
Val Val Tyr Leu Ser Ser Glu Lys Phe Thr Asn Glu Phe Ile Asn Ser		
180	185	190
Ile Arg Asp Asn Lys Ala Val Asp Phe Arg Asn Arg Tyr Arg Asn Val		
195	200	205
Asp Val Leu Leu Ile Asp Asp Ile Gln Phe Leu Ala Gly Lys Glu Gln		
210	215	220
Thr Gln Glu Glu Phe Phe His Thr Phe Asn Thr Leu His Glu Glu Ser		
225	230	235
Lys Gln Ile Val Ile Ser Ser Asp Arg Pro Pro Lys Glu Ile Pro Thr		
245	250	255
Leu Glu Asp Arg Leu Arg Ser Arg Phe Glu Trp Gly Leu Ile Thr Asp		
260	265	270
Ile Thr Pro Pro Asp Leu Glu Thr Arg Ile Ala Ile Leu Arg Lys Lys		
275	280	285
Ala Lys Ala Glu Gly Leu Asp Ile Pro Asn Glu Val Met Leu Tyr Ile		
290	295	300
Ala Asn Gln Ile Asp Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile		
305	310	315
Arg Val Val Ala Tyr Ser Ser Leu Ile Asn Lys Asp Ile Asn Ala Asp		
325	330	335
Leu Ala Ala Glu Ala Leu Lys Asp Ile Ile Pro Ser Ser Lys Pro Lys		
340	345	350
Val Ile Thr Ile Lys Glu Ile Gln Arg Val Val Gly Gln Gln Phe Asn		
355	360	365
Ile Lys Leu Glu Asp Phe Lys Ala Lys Lys Arg Thr Lys Ser Val Ala		
370	375	380
Phe Pro Arg Gln Ile Ala Met Tyr Leu Ser Arg Glu Met Thr Asp Ser		
385	390	395
Ser Leu Pro Lys Ile Gly Glu Glu Phe Gly Gly Arg Asp His Thr Thr		
405	410	415
Val Ile His Ala His Glu Lys Ile Ser Lys Leu Leu Ala Asp Asp Glu		

420

425

430

Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys
 435 440 445

<210> 99
 <211> 507
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 99
 Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
 1 5 10 15

 Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
 20 25 30

 Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu
 35 40 45

 Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
 50 55 60

 Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
 65 70 75 80

 Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
 85 90 95

 Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
 100 105 110

 Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
 115 120 125

 Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
 130 135 140

 His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
 145 150 155 160

 Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
 165 170 175

 Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala
 180 185 190

Ile	Ala	Glu	Ala	Pro	Ala	Arg	Ala	Tyr	Asn	Pro	Leu	Phe	Ile	Trp	Gly
195															205
Glu	Ser	Gly	Leu	Gly	Lys	Thr	His	Leu	Leu	His	Ala	Ala	Gly	Asn	Tyr
210															220
Ala	Gln	Arg	Leu	Phe	Pro	Gly	Met	Arg	Val	Lys	Tyr	Val	Ser	Thr	Glu
225															240
Glu	Phe	Thr	Asn	Asp	Phe	Ile	Asn	Ser	Leu	Arg	Asp	Asp	Arg	Lys	Val
245															255
Ala	Phe	Lys	Arg	Ser	Tyr	Arg	Asp	Val	Asp	Val	Leu	Leu	Val	Asp	Asp
260															270
Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Gly	Ile	Gln	Glu	Glu	Phe	Phe	His
275															285
Thr	Phe	Asn	Thr	Leu	His	Asn	Ala	Asn	Lys	Gln	Ile	Val	Ile	Ser	Ser
290															300
Asp	Arg	Pro	Pro	Lys	Gln	Leu	Ala	Thr	Leu	Glu	Asp	Arg	Leu	Arg	Thr
305															320
Arg	Phe	Glu	Trp	Gly	Leu	Ile	Thr	Asp	Val	Gln	Pro	Pro	Glu	Leu	Glu
325															335
Thr	Arg	Ile	Ala	Ile	Leu	Arg	Lys	Lys	Ala	Gln	Met	Glu	Arg	Leu	Ala
340															350
Val	Pro	Asp	Asp	Val	Leu	Glu	Leu	Ile	Ala	Ser	Ser	Ile	Glu	Arg	Asn
355															365
Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	Arg	Val	Thr	Ala	Phe	Ala	Ser
370															380
Leu	Asn	Lys	Thr	Pro	Ile	Asp	Lys	Ala	Leu	Ala	Glu	Ile	Val	Leu	Arg
385															400
Asp	Leu	Ile	Ala	Asp	Ala	Asn	Thr	Met	Gln	Ile	Ser	Ala	Ala	Thr	Ile
405															415
Met	Ala	Ala	Thr	Ala	Glu	Tyr	Phe	Asp	Thr	Thr	Val	Glu	Glu	Leu	Arg
420															430
Gly	Pro	Gly	Lys	Thr	Arg	Ala	Leu	Ala	Gln	Ser	Arg	Gln	Ile	Ala	Met
435															445

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile
465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
500 505

<210> 100

<211> 446

<212> PRT

<213> Thermus thermophilus

<400> 100

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
145 150 155 160

Phe	Pro	His	Met	Arg	Leu	Glu	Tyr	Val	Ser	Thr	Glu	Thr	Phe	Thr	Asn
			165			170					175				
Glu	Leu	Ile	Asn	Arg	Pro	Ser	Ala	Arg	Asp	Arg	Met	Thr	Glu	Phe	Arg
	180				185						190				
Glu	Arg	Tyr	Arg	Ser	Val	Asp	Leu	Leu	Leu	Val	Asp	Asp	Val	Gln	Phe
	195				200					205					
Ile	Ala	Gly	Lys	Glu	Arg	Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn
	210			215						220					
Ala	Leu	Tyr	Glu	Ala	His	Lys	Gln	Ile	Ile	Leu	Ser	Ser	Asp	Arg	Pro
	225			230			235				240				
Pro	Lys	Asp	Ile	Leu	Thr	Leu	Glu	Ala	Arg	Leu	Arg	Ser	Arg	Phe	Glu
	245				250			255							
Trp	Gly	Leu	Ile	Thr	Asp	Asn	Pro	Ala	Pro	Asp	Leu	Glu	Thr	Arg	Ile
	260				265			270							
Ala	Ile	Leu	Lys	Met	Asn	Ala	Ser	Ser	Gly	Pro	Glu	Asp	Pro	Glu	Asp
	275				280			285							
Ala	Leu	Glu	Tyr	Ile	Ala	Arg	Gln	Val	Thr	Ser	Asn	Ile	Arg	Glu	Trp
	290			295				300							
Glu	Gly	Ala	Leu	Met	Arg	Ala	Ser	Pro	Phe	Ala	Ser	Leu	Asn	Gly	Val
	305			310			315			320					
Glu	Leu	Thr	Arg	Ala	Val	Ala	Lys	Ala	Leu	Arg	His	Leu	Arg	Pro	
	325				330			335							
Arg	Glu	Leu	Glu	Ala	Asp	Pro	Leu	Glu	Ile	Ile	Arg	Lys	Ala	Ala	Gly
	340				345			350							
Pro	Val	Arg	Pro	Glu	Thr	Pro	Gly	Gly	Ala	His	Gly	Glu	Arg	Arg	Lys
	355				360			365							
Lys	Glu	Val	Val	Leu	Pro	Arg	Gln	Leu	Ala	Met	Tyr	Leu	Val	Arg	Glu
	370			375				380							
Leu	Thr	Pro	Ala	Ser	Leu	Pro	Glu	Ile	Gly	Gln	Leu	Phe	Gly	Gly	Arg
	385			390			395			400					
Asp	His	Thr	Thr	Val	Arg	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Ala
	405				410			415							

Gly	Lys	Pro	Asp	Arg	Glu	Val	Gln	Gly	Leu	Leu	Arg	Thr	Leu	Arg	Glu
						420			425					430	
Ala	Cys	Thr	Asp	Pro	Val	Asp	Asn	Leu	Trp	Ile	Thr	Cys	Gly		
						435			440			445			
<210> 101															
<211> 467															
<212> PRT															
<213> Escherichia coli															
<400> 101															
Met	Ser	Leu	Ser	Leu	Trp	Gln	Gln	Cys	Leu	Ala	Arg	Leu	Gln	Asp	Glu
1									10					15	
Leu	Pro	Ala	Thr	Glu	Phe	Ser	Met	Trp	Ile	Arg	Pro	Leu	Gln	Ala	Glu
									25					30	
Leu	Ser	Asp	Asn	Thr	Leu	Ala	Leu	Tyr	Ala	Pro	Asn	Arg	Phe	Val	Leu
									40					45	
Asp	Trp	Val	Arg	Asp	Lys	Tyr	Leu	Asn	Asn	Ile	Asn	Gly	Leu	Leu	Thr
														60	
Ser	Phe	Cys	Gly	Ala	Asp	Ala	Pro	Gln	Leu	Arg	Phe	Glu	Val	Gly	Thr
									65					80	
Lys	Pro	Val	Thr	Gln	Thr	Pro	Gln	Ala	Ala	Val	Thr	Ser	Asn	Val	Ala
									85					95	
Ala	Pro	Ala	Gln	Val	Ala	Gln	Thr	Gln	Pro	Gln	Arg	Ala	Ala	Pro	Ser
									100					110	
Thr	Arg	Ser	Gly	Trp	Asp	Asn	Val	Pro	Ala	Pro	Ala	Glu	Pro	Thr	Tyr
									115					125	
Arg	Ser	Asn	Val	Asn	Val	Lys	His	Thr	Phe	Asp	Asn	Phe	Val	Glu	Gly
									130					140	
Lys	Ser	Asn	Gln	Leu	Ala	Arg	Ala	Ala	Ala	Arg	Gln	Val	Ala	Asp	Asn
									145					160	
Pro	Gly	Gly	Ala	Tyr	Asn	Pro	Leu	Phe	Leu	Tyr	Gly	Gly	Thr	Gly	Leu
									165					175	
Gly	Lys	Thr	His	Leu	Leu	His	Ala	Val	Gly	Asn	Gly	Ile	Met	Ala	Arg

180	185	190
Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln		
195	200	205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg		
210	215	220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe		
225	230	235
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala		
245	250	255
Leu Leu Glu Gly Asn Gln Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro		
260	265	270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp		
275	280	285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala		
290	295	300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu		
305	310	315
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu		
325	330	335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg		
340	345	350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala		
355	360	365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala		
370	375	380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser		
385	390	395
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu		
405	410	415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg		
420	425	430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg		

435

440

445

Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr
450 455 460

Leu Ser Ser
465

<210> 102
<211> 440
<212> PRT
<213> Thermatoga maritima

<400> 102
Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys
1 5 10 15

Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly
20 25 30

Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu
35 40 45

Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu
50 55 60

Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His
65 70 75 80

Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr
85 90 95

Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly
100 105 110

Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly
115 120 125

Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Val Gly Leu Gly Lys Thr
130 135 140

His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp
145 150 155 160

Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val
165 170 175

Asp	Ser	Met	Lys	Glu	Gly	Lys	Leu	Asn	Glu	Phe	Arg	Glu	Lys	Tyr	Arg
		180				185							190		
Lys	Lys	Val	Asp	Ile	Leu	Leu	Ile	Asp	Asp	Val	Gln	Phe	Leu	Ile	Gly
	195				200							205			
Lys	Thr	Gly	Val	Gln	Thr	Glu	Leu	Phe	His	Thr	Phe	Asn	Glu	Leu	His
	210				215					220					
Asp	Ser	Gly	Lys	Gln	Ile	Val	Ile	Cys	Ser	Asp	Arg	Glu	Pro	Gln	Lys
	225				230				235				240		
Leu	Ser	Glu	Phe	Gln	Asp	Arg	Leu	Val	Ser	Arg	Phe	Gln	Met	Gly	Leu
		245				250						255			
Val	Ala	Lys	Leu	Glu	Pro	Pro	Asp	Glu	Glu	Thr	Arg	Lys	Ser	Ile	Ala
		260				265					270				
Arg	Lys	Met	Leu	Glu	Ile	Glu	His	Gly	Glu	Leu	Pro	Glu	Glu	Val	Leu
		275				280					285				
Asn	Phe	Val	Ala	Glu	Asn	Val	Asp	Asp	Asn	Leu	Arg	Arg	Leu	Arg	Gly
	290				295				300						
Ala	Ile	Ile	Lys	Leu	Leu	Val	Tyr	Lys	Glu	Thr	Thr	Gly	Lys	Glu	Val
	305				310			315				320			
Asp	Leu	Lys	Glu	Ala	Ile	Leu	Leu	Lys	Asp	Phe	Ile	Lys	Pro	Asn	
		325				330					335				
Arg	Val	Lys	Ala	Met	Asp	Pro	Ile	Asp	Glu	Leu	Ile	Glu	Ile	Val	Ala
		340				345					350				
Lys	Val	Thr	Gly	Val	Pro	Arg	Glu	Glu	Ile	Leu	Ser	Asn	Ser	Arg	Asn
		355				360					365				
Val	Lys	Ala	Leu	Thr	Ala	Arg	Arg	Ile	Gly	Met	Tyr	Val	Ala	Lys	Asn
		370				375				380					
Tyr	Leu	Lys	Ser	Ser	Leu	Arg	Thr	Ile	Ala	Glu	Lys	Phe	Asn	Arg	Ser
	385				390			395				400			
His	Pro	Val	Val	Val	Asp	Ser	Val	Lys	Lys	Val	Lys	Asp	Ser	Leu	Leu
			405				410					415			
Lys	Gly	Asn	Lys	Gln	Leu	Lys	Ala	Leu	Ile	Asp	Glu	Val	Ile	Gly	Glu
			420				425					430			

Ile Ser Arg Arg Ala Leu Ser Gly
435 440

<210> 103
<211> 457
<212> PRT
<213> Helicobacter pylori

<400> 103
Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
115 120 125

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
130 135 140

Pro Val Leu Phe Tyr Gly Thr Gly Leu Gly Lys Thr His Ile Leu
145 150 155 160

Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
165 170 175

Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
180 185 190

Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
195 200 205

Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu
210 215 220

Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile
225 230 235 240

Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp
245 250 255

Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro
260 265 270

Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu
275 280 285

Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His
290 295 300

Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser
305 310 315 320

Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys
325 330 335

Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu
340 345 350

Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser
355 360 365

Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys
370 375 380

Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser
385 390 395 400

Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met
405 410 415

Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Glu Lys Ser Pro Phe Val
420 425 430

Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp
435 440 445

Lys Lys Thr Ala Phe Asn Ser Ser Glu
450 455

<210> 104
<211> 1305
<212> DNA
<213> Thermus thermophilus

<400> 104
gtgtcgacg aggccgtctg gcaacacgtt ctggagcaca tccgcccag catcaccgag 60
gtggagttcc acacctggtt tgaaggatc cgccccttgg ggatccggga cggggtgctg 120
gagctcgccg tgcccacctc cttgccttg gactggatcc ggcgccacta cgccggcctc 180
atccaggagg gcccctggct ctcggggcc caggcgcccc gtggtagct ccgggtggtg 240
cccggggtcg tagtccagga ggacatctt cagccccccgc cgagcccccc ggcccaagct 300
caacccgaag ataccttaa aacttcgtgg tggggcccaa caactccatg gccccacggc 360
ggcgccgtgg ccgtggccga gtccccccgc cgggcctaca acccccctt catctacggg 420
ggccgtggcc tggaaagac ctacctgtatg cacgcccgtgg gcccaactccg tgcgaagcgc 480
ttccccaca tgagattaga gtacgtttcc acggaaactt tcaccaacga gctcatcaac 540
cgcccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtggacctc 600
ctgctggtgg acgacgtcca gtcatecgcc ggaaaggagc gcacccagga ggagttttc 660
cacacccatca acgcccccta cgaggcccac aagcagatca tcctctccctc cgaccggccg 720
cccaaggaca tcctcaccct ggaggcgcgc ctgcggagcc gtttgagtg gggctgatc 780
accgacaatc cagccccca cctggaaacc cggatcgcca tcctgaagat gaacgccagc 840
agcgggcctg agatcccga ggacgcccctg gtagtacatcg cccggcaggt cacctccaa 900
atccggagtg gggaaaggggc cctcatgcgg gcatcgccct tcgcctccct caacggcggt 960
gagctgaccc gcgccgtggc ggccaaggct ctccgacatc ttccggccag ggagctggag 1020
gcggaccctt tggagatcat ccgcaaagcg gcgggaccag ttccggctga aacccggga 1080
ggagctcacg gggagcgcgc caagaaggag tgggtccctcc cccggcagct cgccatgtac 1140
ctgggtcgccg agtcacccctt ggccctccctg cccgagatcg accagctcaa cgacgaccgg 1200
gaccacacca cggtcctcta cggccatccag aagggtccagg agtcgcggg aagcgaccgg 1260
gagggtgcagg gcctccctccg caccctccgg gaggcgtgca catga 1305

<210> 105
<211> 434
<212> PRT
<213> Thermus thermophilus

<400> 105
Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly

50	55	60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val		
65	70	75
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro		
85	90	95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly		
100	105	110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser		
115	120	125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu		
130	135	140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg		
145	150	155
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn		
165	170	175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg		
180	185	190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe		
195	200	205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn		
210	215	220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro		
225	230	235
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu		
245	250	255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile		
260	265	270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp		
275	280	285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp		
290	295	300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val		

305	310	315	320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro			
325	330	335	
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly			
340	345	350	
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys			
355	360	365	
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu			
370	375	380	
Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg			
385	390	395	400
Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala			
405	410	415	
Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala			
420	425	430	

Cys Thr

<210> 106
<211> 1128
<212> DNA
<213> Thermus thermophilus

<400> 106
atgaacataa cggttcccaa aaaactcctc tcggaccagc tttccctcct ggagcgcatc 60
gtcccctcta gaagcgccaa ccccctctac acctacctgg ggctttacgc cgaggaaggg 120
gccttgcattc tcttcgggac caacggggag gtggacctcg aggtccgcct ccccgccgag 180
gccccaaagcc ttccccgggt gctcgccccccc gcccagccct tcttccagct ggtgcggagc 240
cttcctgggg acctcggtgc ctcggccctc gcctcgaggc cgggccaggg gggcagctg 300
gagctctcct ccggcggtt ccgcacccgg ctcagcctgg cccctgccga gggctacccc 360
gagcttctgg tgccccgggg ggaggacaag ggggccttcc ccctccggac gcgatgccc 420
tccggggagc tcgtcaaggc cttgacccac gtgcgtacg ccgcgagcaa cgaggagtac 480
cgggccatct tccgcggggt gcagctggag ttctcccccc agggcttccg ggccgtggcc 540
tccgacgggt accgcctcgc cctctacgac ctgccccctgc cccaagggtt ccaggccaag 600
gccgtggtcc cccggccggag cgtggacgag atggtgccgg tccctgaaggg ggcggacggg 660
gccgaggccg tcctcgccct gggcgagggg gtgttggccc tqqccctcga gggcggaaagc 720
ggggtccgga tggccctccg cctcatggaa ggggagttcc ccgactacca gagggtcatc 780
ccccaggagt tcgcccctcaa ggtccaggtg gagggggagg ccctcaggga ggcggtgccgc 840
cgggtgagcg tcctctccga cccgcagaac caccgggtgg acctccttt ggaggaaggc 900

cggatcctcc tctccgccga gggggactac ggcaaggggc aggaggaggt gcccgcggc 960
gtggaggggc cggacatggc cgtggcctac aacgcccgt acctcctcga ggccctcgcc 1020
cccggtgggg accggggcca cctgggcata tccgggcca cgagccccgag cctcatctgg 1080
ggggacgggg aggggtaccg ggcggtggtg gtgccccta gggcttag 1128

<210> 107
<211> 376
<212> PRT
<213> Thermus thermophilus

<400> 107
Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
35 40 45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
50 55 60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
65 70 75 80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
85 90 95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
100 105 110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
115 120 125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
130 135 140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
145 150 155 160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
165 170 175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
180 185 190

Leu	Pro	Gln	Gly	Phe	Gln	Ala	Lys	Ala	Val	Val	Pro	Ala	Arg	Ser	Val
195						200					205				
Asp	Glu	Met	Val	Arg	Val	Leu	Lys	Gly	Ala	Asp	Gly	Ala	Glu	Ala	Val
210					215					220					
Leu	Ala	Leu	Gly	Glu	Gly	Val	Leu	Ala	Leu	Ala	Leu	Glu	Gly	Gly	Ser
225						230				235				240	
Gly	Val	Arg	Met	Ala	Leu	Arg	Leu	Met	Glu	Gly	Glu	Phe	Pro	Asp	Tyr
245							250					255			
Gln	Arg	Val	Ile	Pro	Gln	Glu	Phe	Ala	Leu	Lys	Val	Gln	Val	Glu	Gly
260							265				270				
Glu	Ala	Leu	Arg	Glu	Ala	Val	Arg	Arg	Val	Ser	Val	Leu	Ser	Asp	Arg
275						280				285					
Gln	Asn	His	Arg	Val	Asp	Leu	Leu	Leu	Glu	Glu	Gly	Arg	Ile	Leu	Leu
290					295				300						
Ser	Ala	Glu	Gly	Asp	Tyr	Gly	Lys	Gly	Gln	Glu	Glu	Val	Pro	Ala	Gln
305					310				315			320			
Val	Glu	Gly	Pro	Asp	Met	Ala	Val	Ala	Tyr	Asn	Ala	Arg	Tyr	Leu	Leu
325							330				335				
Glu	Ala	Leu	Ala	Pro	Val	Gly	Asp	Arg	Ala	His	Leu	Gly	Ile	Ser	Gly
340						345				350					
Pro	Thr	Ser	Pro	Ser	Leu	Ile	Trp	Gly	Asp	Gly	Glu	Gly	Tyr	Arg	Ala
355						360				365					
Val	Val	Val	Pro	Leu	Arg	Val	Glx								
370					375										
<210> 108															
<211> 376															
<212> PRT															
<213> Thermus thermophilus															
<400> 108															
Met	Asn	Ile	Thr	Val	Pro	Lys	Lys	Leu	Leu	Ser	Asp	Gln	Leu	Ser	Leu
1					5				10			15			
Leu	Glu	Arg	Ile	Val	Pro	Ser	Arg	Ser	Ala	Asn	Pro	Leu	Tyr	Thr	Tyr
20						25					30				

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
35 40 45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
50 55 60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
65 70 75 80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
85 90 95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
100 105 110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
115 120 125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
130 135 140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
145 150 155 160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
165 170 175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
180 185 190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
195 200 205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
210 215 220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Ser
225 230 235 240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
245 250 255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
260 265 270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300

 Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

 Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

 Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

 Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

 Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 109
 <211> 367
 <212> PRT
 <213> Escherichia coli

<400> 109
 Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15

 Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30

 Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45

 Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
 50 55 60

 Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
 65 70 75 80

 Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
 85 90 95

 Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110

 Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115	120	125
Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe		
130	135	140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe		
145	150	155
Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg		
165	170	175
Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser		
180	185	190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp		
195	200	205
Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg		
210	215	220
Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg		
225	230	235
Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu		
245	250	255
Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile		
260	265	270
Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn		
275	280	285
Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu		
290	295	300
Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn		
305	310	315
Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val		
325	330	335
Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala		
340	345	350
Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx		
355	360	365

<210> 110
<211> 367
<212> PRT
<213> Proteus mirabilis

<400> 110
Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln
1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
20 25 30

Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu
50 55 60

Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg
65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg
85 90 95

Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100 105 110

Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115 120 125

Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe
130 135 140

Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145 150 155 160

Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165 170 175

Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser
180 185 190

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp
195 200 205

Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu
210 215 220

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
225 230 235 240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
245 250 255

Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
260 265 270

Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
275 280 285

Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
290 295 300

Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
325 330 335

Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
340 345 350

Val Ala Ser Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
355 360 365

<210> 111
<211> 366
<212> PRT
<213> Haemophilus influenzae

<400> 111
Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
1 5 10 15

Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
20 25 30

Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp
35 40 45

Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Glu
50 55 60

Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg
65 70 75 80

Thr Leu Ser Asp Asp Ser Glu Ile Thr Val Thr Phe Glu Gln Asp Arg
 85 90 95

 Ala Leu Val Gln Ser Gly Arg Ser Arg Phe Thr Leu Ala Thr Gln Pro
 100 105 110

 Ala Glu Glu Tyr Pro Asn Leu Thr Asp Trp Gln Ser Glu Val Asp Phe
 115 120 125

 Glu Leu Pro Gln Asn Thr Leu Arg Arg Leu Ile Glu Ala Thr Gln Phe
 130 135 140

 Ser Met Ala Asn Gln Asp Ala Arg Tyr Phe Leu Asn Gly Met Lys Phe
 145 150 160

 Glu Thr Glu Gly Asn Leu Leu Arg Thr Val Ala Thr Asp Gly His Arg
 165 170 175

 Leu Ala Val Cys Thr Ile Ser Leu Glu Gln Glu Leu Gln Asn His Ser
 180 185 190

 Val Ile Leu Pro Arg Lys Gly Val Leu Glu Leu Val Arg Leu Leu Glu
 195 200 205

 Thr Asn Asp Glu Pro Ala Arg Leu Gln Ile Gly Thr Asn Asn Leu Arg
 210 215 220

 Val His Leu Lys Asn Thr Val Phe Thr Ser Lys Leu Ile Asp Gly Arg
 225 230 240

 Phe Pro Asp Tyr Arg Arg Val Leu Pro Arg Asn Ala Thr Lys Ile Val
 245 250 255

 Glu Gly Asn Trp Glu Met Leu Lys Gln Ala Phe Ala Arg Ala Ser Ile
 260 265 270

 Leu Ser Asn Glu Arg Ala Arg Ser Val Arg Leu Ser Leu Lys Glu Asn
 275 280 285

 Gln Leu Lys Ile Thr Ala Ser Asn Thr Glu His Glu Glu Ala Glu Glu
 290 295 300

 Ile Val Asp Val Asn Tyr Asn Gly Glu Glu Leu Glu Val Gly Phe Asn
 305 310 320

 Val Thr Tyr Ile Leu Asp Val Leu Asn Ala Leu Lys Cys Asn Gln Val
 325 330 335

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
 340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
 355 360 365

<210> 112
 <211> 367
 <212> PRT
 <213> *Pseudomonas putida*

<400> 112
 Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
 1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
 20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
 50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
 65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
 85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
 100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
 115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
 130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
 165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His

180	185	190
Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu		
195	200	205
Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile		
210	215	220
Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly		
225	230	235
Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu		
245	250	255
Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala		
260	265	270
Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala		
275	280	285
Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu		
290	295	300
Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe		
305	310	315
Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln		
325	330	335
Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu		
340	345	350
Ala Gly Asn Asp Asp Ser Ser Tyr Val Val Met Pro Met Arg Leu		
355	360	365
<210> 113		
<211> 366		
<212> PRT		
<213> Buchnera aphidicola		
<400> 113		
Met Lys Phe Thr Ile Gln Asn Asp Ile Leu Thr Lys Asn Leu Lys Lys		
1	5	10
15		
Ile Thr Arg Val Leu Val Lys Asn Ile Ser Phe Pro Ile Leu Glu Asn		
20	25	30

Ile	Leu	Ile	Gln	Val	Glu	Asp	Gly	Thr	Leu	Ser	Leu	Thr	Thr	Thr	Asn
								35				40			45
Leu	Glu	Ile	Glu	Leu	Ile	Ser	Lys	Ile	Glu	Ile	Ile	Thr	Lys	Tyr	Ile
	50					55						60			
Pro	Gly	Lys	Thr	Thr	Ile	Ser	Gly	Arg	Lys	Ile	Leu	Asn	Ile	Cys	Arg
	65						70			75			80		
Thr	Leu	Ser	Glu	Lys	Ser	Lys	Ile	Lys	Met	Gln	Leu	Lys	Asn	Lys	Lys
				85					90				95		
Met	Tyr	Ile	Ser	Ser	Glu	Asn	Ser	Asn	Tyr	Ile	Leu	Ser	Thr	Leu	Ser
				100				105				110			
Ala	Asp	Thr	Phe	Pro	Asn	His	Gln	Asn	Phe	Asp	Tyr	Ile	Ser	Lys	Phe
	115						120				125				
Asp	Ile	Ser	Ser	Asn	Ile	Leu	Lys	Glu	Met	Ile	Glu	Lys	Thr	Glu	Phe
	130					135				140					
Ser	Met	Gly	Lys	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Leu
	145					150				155			160		
Glu	Lys	Asp	Lys	Phe	Leu	Arg	Ser	Val	Ala	Thr	Asp	Gly	Tyr	Arg	
	165					170				175					
Leu	Ala	Ile	Ser	Tyr	Thr	Gln	Leu	Lys	Asp	Ile	Asn	Phe	Phe	Ser	
				180			185				190				
Ile	Ile	Ile	Pro	Asn	Lys	Ala	Val	Met	Glu	Leu	Leu	Lys	Leu	Leu	Asn
				195			200				205				
Thr	Gln	Pro	Gln	Leu	Leu	Asn	Ile	Leu	Ile	Gly	Ser	Asn	Ser	Ile	Arg
	210				215				220						
Ile	Tyr	Thr	Lys	Asn	Leu	Ile	Phe	Thr	Thr	Gln	Leu	Ile	Glu	Gly	Glu
	225					230				235			240		
Tyr	Pro	Asp	Tyr	Lys	Ser	Val	Leu	Phe	Lys	Glu	Lys	Lys	Asn	Pro	Ile
			245				250				255				
Ile	Thr	Asn	Ser	Ile	Leu	Leu	Lys	Ser	Leu	Leu	Arg	Val	Ala	Ile	
				260			265				270				
Leu	Ala	His	Glu	Lys	Phe	Cys	Gly	Ile	Glu	Ile	Lys	Ile	Glu	Asn	Gly
			275			280				285					

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
290 295 300

Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
305 310 315 320

Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
325 330 335

Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu
340 345 350

Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
355 360 365

<210> 114

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 114

gtgtggatcc tcgtccccct catgcgcgac caggaagg

39

<210> 115

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 115

gtgtggatcc gtggtgacct tagccac

27

<210> 116

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 116
ttcgtgtccg aggacaccttggtccacaac

30

<210> 117
<211> 3514
<212> DNA
<213> Aquifex aeolicus

<400> 117
at gagtaagg attcgtcca cttcacctg cacaccagt tctcactcct ggacgggct 60
ataaaagatag acgagctcgtaaaaaaggca aaggagtatg gatacaaagc tgtcgaaatg 120
tcagaccacg gaaacctctt cggttcgtat aaattctaca aagccctgaa ggcggaagga 180
attaagccca taatcggcat ggaagcctac tttaccacgg gttcgaggtt tgacagaaaag 240
actaaaacga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatagca 300
aaggacgaaa aggtctaaag aacttaatga agctctcaac cctcgcc tacaaagaagg 360
tttactacaa acccagaatt gattacgaac tccttggaaaa gtacggggag ggcctaata 420
cccttaccgc atgcctgaaa ggtgttccc cctactacgc ttctataaac gaagtggaaa 480
aggcggagga atgggtaaaag aagttcaagg atatattcgg agatgacctt tatttagaac 540
ttcaagcga caacattcca gaacaggaag tggcaaacag gaacttaata gagatagcca 600
aaaagtacga tgtgaaactc atagcgacgc aggacgccc ctacctcaat cccgaagaca 660
gttacgccc cacgggtctt atggcacttc aaatggggaaa gaccattcac gaactgagtt 720
cgggaaactt caagtgttca aacgaagacc ttcactttgc tccacccgag tacatgtgga 780
aaaagttga aggttaagttc gaaggctggg aaaaggcact cctgaacact ctcgaggtaa 840
tggaaaagac agcggacacg tttgagatat ttgaaaactc cacctaccc tttcccaagt 900
acgacgttcc gcccgcacaaa acccttgagg aatacctcag agaactcgcg tacaaagg 960
taagacagag gatagaaaagg ggacaagcta aggatactaa agagtactgg gagaggctg 1020
agtacgaact ggaagttata aacaaaatgg gctttgcggg atacttcttgc atagttcagg 1080
acttcataaa ctgggctaag aaaaacgaca tacctgttgg accccggaaagg ggaagtgcgt 1140
gaggttccct cgtcgcatac gccatcgaa taacggacgt tgaccctata aagcacggat 1200
tccttttga gaggttctt aaccccgaaa gggttccat gccggatata gacgtggatt 1260
tctgtcagga caacaggaa aaggtcatag agtacgtaa gaacaagtac ggacacgaca 1320
acgtagctca gataatcacc tacaacgtaa tgaaggcgaa gcaaacaactg agagacgtcg 1380
caagggccat gggactcccc tactccaccg cggacaaaactc cgcaaaaactc attcctcagg 1440
gggacgttca gggacgtgg ctcagtctgg aagagatgtaa caaaacgcct gtggaggaac 1500
tccttcagaa gtacggagaa cacagaacgg acatagagga caacgtaaag aagttcagac 1560
agatatgcga agaaagtccg gagataaaac agtcgttga gacggccctg aagcttgaag 1620
gtctcacgag acacacccctt ccacacccg cgggagtggt tatagcacca aagcccttga 1680
gcgagctcgtaccc tacgataaaag agggcgaagt cgcaaccagg tacgacatgg 1740
ttcagctcga agaactcggt ctccctgaaga tggacttctt cggactcaaa accctcacag 1800
aactgaaact catgaaagaa ctcataaagg aaagacacgg agtggatata aacttccttgc 1860
aacttccctt tgacgacccg aaagtttaca aactccttca ggaaggaaaa accacgggag 1920
tgttccagct cgaaacgcagg ggaatgaaag aactcctgaa gaaactaaag cccgacagct 1980
ttgacgacat cggtgcggtc ctcgcactct acagacccgg acctctaaag agcggactcg 2040
ttgacacata cattaagaga aagcacggaa aagaacccgt tgagtacccc ttcccgagc 2100
ttgaacccgt ccttaaggaa acctacggag taatcgttta tcaggaacag gtatgaa 2160
tgtctcagat actttccggc tttactcccg gagaggcgga taccctcaga aaggcgatag 2220
gtaagaagaa agcggattta atggctcaga tgaaagacaa gttcatacag ggagcggtgg 2280

aaagggata ccctgaagaa aagataagga agctctggga agacatagag aagttcgctt 2340
cctactcctt caacaagtct cactcggtag cttacggta catctcctac tggaccgcct 2400
acgttaaagc ccactatccc gcggagttct tcgcgtaaa actcacaact gaaaagaacg 2460
acaacaagtt cctcaacctc ataaaagacg ctaaactctt cgatttgag atacttcccc 2520
ccgacataaa caagagtat gttaggattt cgatagaagg tgaaaacagg ataaggttcg 2580
ggcttcgag gataaaggga gtggagagg aaactgctaa gataatcgaa gaagctgaa 2640
agaagtataa gcagttcaaa gggcttcgg acttcataaa caaaaaccaag aacaggaaga 2700
taaacaagaa agtcgtggaa gcactcgta aggcaggggc ttttacttt actaagaaaa 2760
agagggaaaga actactcgct aaagtggcaa actctgaaaa agcattaatg gctacacaaa 2820
actcccttt cggcgcaccg aaagaagaag tggagaact cgaccctta aagcttgcgg 2880
aggaagttct cggttttac atttcagggc acccccttga caactacgaa aagctcctca 2940
agaaccgcta cacaccatt gaagatttag aagagtggga caaggaaagc gaagcggtgc 3000
ttacaggagt tatcacggaa ctcaaaagtaa aaaagacgaa aaacggagat tacatggcgg 3060
tcttcaacct cgttgacaag acgggactaa tagagtgtgt cgtcttcccg ggagtttacg 3120
aagaggcaaa ggaactgata gaagaggaca gagtagtggg agtcaaaggt tttctggacg 3180
aggaccttga aacggaaaaat gtcaagttcg tggtaaaga ggtttctcc cctgaggagt 3240
tcgcaagga gatgaggaat acccttata tattctaaa aagagagcaa gccctaaacg 3300
gcgttgcga aaaactaaag ggaattattt aaaaacaacag gacggaggac ggatacaact 3360
tggttctcac ggttgatctg ggagactact tcgttgattt agcactccca caagatatga 3420
aactaaaggc tgacagaaaag gttgttaggg agatagaaaa actgggagtg aaggtcataa 3480
tttagtaat aacccttact tccgagtagt cccc 3514

<210> 118
<211> 1161
<212> PRT
<213> Aquifex aeolicus

<400>	118														
Met	Ser	Lys	Asp	Phe	Val	His	Leu	His	Leu	His	Thr	Gln	Phe	Ser	Leu
1															15
Leu	Asp	Gly	Ala	Ile	Lys	Ile	Asp	Glu	Leu	Val	Lys	Lys	Ala	Lys	Glu
20															30
Tyr	Gly	Tyr	Lys	Ala	Val	Gly	Met	Ser	Asp	His	Gly	Asn	Leu	Phe	Gly
35															45
Ser	Tyr	Lys	Phe	Tyr	Lys	Ala	Leu	Lys	Ala	Glu	Gly	Ile	Lys	Pro	Ile
50															60
Ile	Gly	Met	Glu	Ala	Tyr	Phe	Thr	Thr	Gly	Ser	Arg	Phe	Asp	Arg	Lys
65															80
Thr	Lys	Thr	Ser	Glu	Asp	Asn	Ile	Thr	Asp	Lys	Tyr	Asn	His	His	Leu
															95
Ile	Leu	Ile	Ala	Lys	Asp	Asp	Lys	Gly	Leu	Lys	Asn	Leu	Met	Lys	Leu

100	105	110
Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp		
115	120	125
Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala		
130	135	140
Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys		
145	150	155
Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp		
165	170	175
Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala		
180	185	190
Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile		
195	200	205
Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His		
210	215	220
Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser		
225	230	235
240		
Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro		
245	250	255
Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys		
260	265	270
Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe		
275	280	285
Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro		
290	295	300
Pro Asp Lys Thr Leu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly		
305	310	315
320		
Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr		
325	330	335
Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe		
340	345	350
Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys		

355	360	365
Asn Asp Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Gly Gly Ser Leu		
370	375	380
Val Ala Tyr Ala Ile Gly Ile Thr Asp Val Asp Pro Ile Lys His Gly		
385	390	395
Phe Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp		
405	410	415
Ile Asp Val Asp Phe Cys Gln Asp Asn Arg Glu Lys Val Ile Glu Tyr		
420	425	430
Val Arg Asn Lys Tyr Gly His Asp Asn Val Ala Gln Ile Ile Thr Tyr		
435	440	445
Asn Val Met Lys Ala Lys Gln Thr Leu Arg Asp Val Ala Arg Ala Met		
450	455	460
Gly Leu Pro Tyr Ser Thr Ala Asp Lys Leu Ala Lys Leu Ile Pro Gln		
465	470	475
Gly Asp Val Gln Gly Thr Trp Leu Ser Leu Glu Glu Met Tyr Lys Thr		
485	490	495
Pro Val Glu Glu Leu Leu Gln Lys Tyr Gly Glu His Arg Thr Asp Ile		
500	505	510
Glu Asp Asn Val Lys Lys Phe Arg Gln Ile Cys Glu Glu Ser Pro Glu		
515	520	525
Ile Lys Gln Leu Val Glu Thr Ala Leu Lys Leu Glu Gly Leu Thr Arg		
530	535	540
His Thr Ser Leu His Ala Ala Gly Val Val Ile Ala Pro Lys Pro Leu		
545	550	555
Ser Glu Leu Val Pro Leu Tyr Tyr Asp Lys Glu Gly Glu Val Ala Thr		
565	570	575
Gln Tyr Asp Met Val Gln Leu Glu Glu Leu Gly Leu Leu Lys Met Asp		
580	585	590
Phe Leu Gly Leu Lys Thr Leu Thr Glu Leu Lys Leu Met Lys Glu Leu		
595	600	605
Ile Lys Glu Arg His Gly Val Asp Ile Asn Phe Leu Glu Leu Pro Leu		

610	615	620
Asp Asp Pro Lys Val Tyr Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly		
625	630	635
Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu		
645	650	655
Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg		
660	665	670
Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys		
675	680	685
His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val		
690	695	700
Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys		
705	710	715
Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu		
725	730	735
Arg Lys Ala Ile Gly Lys Lys Ala Asp Leu Met Ala Gln Met Lys		
740	745	750
Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys		
755	760	765
Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe		
770	775	780
Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala		
785	790	795
Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr		
805	810	815
Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys		
820	825	830
Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val		
835	840	845
Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg		
850	855	860
Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg		

865	870	875	880
Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr			
885	890	895	
Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala			
900	905	910	
Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys			
915	920	925	
Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe			
930	935	940	
Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu			
945	950	955	960
Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr			
965	970	975	
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu			
980	985	990	
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu			
995	1000	1005	
Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu			
1010	1015	1020	
Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr			
1025	1030	1035	1040
Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Lys			
1045	1050	1055	
Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val			
1060	1065	1070	
Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr			
1075	1080	1085	
Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu			
1090	1095	1100	
Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn			
1105	1110	1115	1120
Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu			

1125

1130

1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile
1155 1160

<210> 119
<211> 2408
<212> DNA
<213> Aquifex aeolicus

<400> 119
atgaactacg ttcccttcgc gagaaagtac agaccgaaat tcttcaggg a gtaatagga 60
cagaagctc ccgtaggat actcaaaaac gctataaaaa acgacagagt ggctcacgcc 120
tacctcttg ccggaccgag gggggttggg aagacgacta ttgcaagaat tctcgcaaaa 180
gcttgaact gtaaaaatcc ctccaaaggt gagccctgct gtgagtgcga aaactgcagg 240
gagatagaca ggggtgtgtt ccctgactta attgaaaatgg atgcccgcctc aaacaggggt 300
atagacgacg taaggccatt aaaagaagcg gtcaattaca aacctataaa aggaaagtac 360
aaggttaca taatagacga agctcacatg ctcacgaaag aagcttcaa cgctctcta 420
aaaaccctcg aagagcccc tcccagaact gtttcgtcc tttgtaccac ggagtacgac 480
aaaattctc ccacgatact ctcaagggtt cagaggataa tcttctcaaa ggttaagaaag 540
gaaaaagtaa tagagtatct aaaaaagata tgtaaaaagg aaggattga gtgcgaagag 600
ggagcccttg aggttctggc tcatgcctct gaagggtgca tgaggatgc agcctctctc 660
ctggaccagg cgagcggtta cggggaaaggc agggtaacaa aagaagttagt ggagaacttc 720
ctcggattc tcagttagga aagcgtagg agtttctga aattgcttct gaactcagaa 780
gtggacgaag ctataaagtt cctcagagaa ctctcagaaa agggctacaa cctgaccaag 840
tttgggaga tggtaagaaga ggaagtgaga aacgcattt tagtaaagag cctgaaaaat 900
ccgaaagcg tggttcagaa ctggcaggat tacgaagact tcaaagacta ccctctggaa 960
gccctcctct acgttgagaa cctgataaac agggtaaag ttgaagcgag aacgagagaa 1020
cccttaagag ccttgaact cgcgtataa aagagccta tagtcaaaga cataattccc 1080
gtatcccagc tcggaaagtgt ggttaaggaa accaaaaagg aagaaaagaa agttgaagta 1140
aaagaagagc caaaaagtaa agaagaaaaa ccaaaggagc aggaagagga caggttccag 1200
aaagtttaa acgcttgaa cggcaaaatc cttaaaagaa tacttgaagg ggcaaaaagg 1260
gaagaaagag acggaaaaat cgtcctaaag atagaagcct cttatctgag aaccatgaaa 1320
aagaatttg actcaactaa ggagactttt ctttttttag agttgaacc cgtggaggat 1380
aaaaaaaaac ctcagaagtc cagcgggacg aggctgtttt aaaggtaaag gagctcttca 1440
atgcaaaaat actcaaagta cgaagtaaaa gctaaggtaa taaaggtgag aatgcccgtg 1500
gaagagatag ggctgtttaa cgcactaata gacggcttc ccaggtacgc actcacgagg 1560
acgaaggaaa agggaaagg agaagtttc gtttagcga ctccttataa agtcaaggaa 1620
ttgatgaaag ctatggagg tatgaaaaaa cacataaagg atttagaaat cctcggagag 1680
acggatgagg atttaacttt ttaaagtatg ggtgtatctg agcaaaggat taagctaaaa 1740
acaaacctga aacccgcagg ggaccagccg aaagccataa aaaaactcct tgaaaaccta 1800
agggaaaggcg taaaagaaca aacacttctc ggagtcacgg gaagcggaaa gactttact 1860
ctagcaaacg taatagcgaa gtacaacaaa ccaactcttgc ttgttagttca caacaaaatt 1920
ctcgccggcac agctatacag ggagttaaa gaactattcc ctgaaaacgc tgtagagtc 1980

tttgtctt actacgacta ttaccaacct gaagcctaca ttcccgaaaa agatttatac 2040
atagaaaagg acgcgagtat aaacgaaagc tggaacgttt cagacactcc gccacgatat 2100
ccgttctaga aaggaggggac gttatagttag ttgcttcagt ttcttgata tacggactcg 2160
ggaaacctga gcactacgaa aacctgagga taaaactcca aaggggaaata agactgaact 2220
ttagtaagct cctgaggaaa ctcgttgagc taggatatca gagaaatgac tttgccataa 2280
agagggctac cttctcggtt aggggagacg tgggtgagat agtcccttct cacacggaag 2340
attacctcgt gagggttagag ttctgggacg acgaagttga aagaatagtc ctcatggacg 2400
ctctgaac 2408

<210> 120

<211> 473

<212> PRT

<213> Aquifex aeolicus

<400> 120

Met Asn Tyr Val Pro Phe Ala Arg Lys Tyr Arg Pro Lys Phe Phe Arg
1 5 10 15

Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
20 25 30

Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
35 40 45

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
50 55 60

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
65 70 75 80

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
85 90 95

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
100 105 110

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
115 120 125

His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
145 150 155 160

Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
165 170 175

Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
180 185 190

Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
195 200 205

Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
210 215 220

Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
225 230 235 240

Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
245 250 255

Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
260 265 270

Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
275 280 285

Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
290 295 300

Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
305 310 315 320

Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
325 330 335

Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
340 345 350

Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
355 360 365

Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
370 375 380

Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
385 390 395 400

Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
405 410 415

Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
420 425 430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
435 440 445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro
450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe
465 470

<210> 121

<211> 1090

<212> DNA

<213> Aquifex aeolicus

<400> 121

atgcgcgtta aggtggacag ggaggagctt gaagaggttc taaaaaaagc aagagaaagc 60
acgaaaaaaaaa aagccgcact cccgatactc gcgaacttct tactctccgc aaaagaggaa 120
aacatcatcg taagggcaac ggacttggaa aactacctt tagtctccgt aaagggggag 180
gttgaagagg aaggagaggt ttgcgtccac tctcaaaaac tctacgatat agtcaagaac 240
ttaaattccg cttacgttta ctttcatacg gaagggtgaaa aactcgtcat aacgggagga 300
aagagtacgt acaaacttcc gacagctccc gcggaggact ttccgaatt tccagaaatc 360
gtagaaggag gagaaacact ttcgggaaac cttctcgta acggaataga aaaggttagag 420
tacccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatac 480
gaggacagaa ttcactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540
taaacattga aaagagtgaa gacgagtctt ttgcttactt ctccactccc gagtgaaac 600
tcgccgttag ctcctggaag gagaattccc ggactacatg agtgcatacc ctgaggagtt 660
ttcggcggaa gtcttggggaa agacagagga agtcttaaag gttttaaaga ggttgaaac 720
tttaagcgaa gggaaatgtt ttccctgtgaa gattacctt agcggaaacc ttgcacatctt 780
ttagttcgcg gatccggagt tccggagaagc gagagaggaa attgaagtgg agtacacggg 840
agagccctt gagataggat tcaacggaaa taccttatgg aggcgcttga cgctacgac 900
agcgaaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960
gattacgaaa aggaaccta caagtgcata ataatgccga tgagggtgta gccatgaaaa 1020
aagcttaat cttttattt agcttggacc tttaattcc tgcgtttagc gaagccaaac 1080
ccaagtcttc 1090

<210> 122

<211> 363

<212> PRT

<213> Aquifex aeolicus

<400> 122

Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Glu Val Leu Lys Lys
1 5 10 15

Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn

20

25

30

Phe Leu Leu Ser Ala Lys Glu Glu Asn Leu Ile Val Arg Ala Thr Asp
 35 40 45

Leu Glu Asn Tyr Leu Val Val Ser Val Lys Gly Glu Val Glu Glu Glu
 50 55 60

Gly Glu Val Cys Val His Ser Gln Lys Leu Tyr Asp Ile Val Lys Asn
 65 70 75 80

Leu Asn Ser Ala Tyr Val Tyr Leu His Thr Glu Gly Glu Lys Leu Val
 85 90 95

Ile Thr Gly Gly Lys Ser Thr Tyr Lys Leu Pro Thr Ala Pro Ala Glu
 100 105 110

Asp Phe Pro Glu Phe Pro Glu Ile Val Glu Gly Gly Glu Thr Leu Ser
 115 120 125

Gly Asn Leu Leu Val Asn Gly Ile Glu Lys Val Glu Tyr Ala Ile Ala
 130 135 140

Lys Glu Glu Ala Asn Ile Ala Leu Gln Gly Met Tyr Leu Arg Gly Tyr
 145 150 155 160

Glu Asp Arg Ile His Phe Val Gly Ser Asp Gly His Arg Leu Ala Leu
 165 170 175

Tyr Glu Pro Leu Gly Glu Phe Ser Lys Glu Leu Leu Ile Pro Arg Lys
 180 185 190

Ser Leu Lys Val Leu Lys Lys Leu Ile Thr Gly Ile Glu Asp Val Asn
 195 200 205

Ile Glu Lys Ser Glu Asp Glu Ser Phe Ala Tyr Phe Ser Thr Pro Glu
 210 215 220

Trp Lys Leu Ala Val Arg Leu Leu Glu Gly Glu Phe Pro Asp Tyr Met
 225 230 235 240

Ser Val Ile Pro Glu Glu Phe Ser Ala Glu Val Leu Phe Glu Thr Glu
 245 250 255

Glu Val Leu Lys Val Leu Lys Arg Leu Lys Ala Leu Ser Glu Gly Lys
 260 265 270

Val Phe Pro Val Lys Ile Thr Leu Ser Glu Asn Leu Ala Ile Phe Glu

275

280

285

Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu
290 295 300

Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met
305 310 315 320

Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr
325 330 335

Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu
340 345 350

Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val
355 360

<210> 123

<211> 1093

<212> DNA

<213> Aquifex aeolicus

<400> 123

gtggaaacca caatattcca gttccagaaa actttttca caaaacctcc gaaggagagg 60
gtttcgtcc ttcatggaga agagcgttat ctcataagaa ccttttgtc taagctgaag 120
gaaaaagtacg gggagaatta cacggttctg tggggggatg agataagcga ggaggaattc 180
tacactgccc tttccgagac cagtatattc ggcggttcaa aggaaaaaagc ggtggtcatt 240
tacaacttcg gggatttcct gaagaagctc ggaagaaga aaaagggaaa agaaaggctt 300
ataaaaagtcc tcagaaaacgt aaagagtaac tacgtattta tagtgtacga tgcgaaactc 360
cagaaaacagg aactttcttc ggaacctctg aaatccgtag cgtcttcgg cggtatagtg 420
gtagcaaaca ggctgagcaa ggagaggata aaacagctcg tccttaagaa gttcaaagaa 480
aaaggataa acgtagaaaa cgtgccctt gaataccctc tccagctcac gggttacaac 540
ttgatggagc tcaaacttga ggttggaaaa ctgatagatt acgcaagtga aaagaaaatt 600
ttaacactcg atgaggtaaa gagagtagcc ttctcagtct cagaaaacgt aaacgtatTTT 660
gagttcgttg atttactcct cttaaaagat tacgaaaagg ctcttaaagt tttggactcc 720
ctcatttcct tcggaataaca cccccctccag attatggaaaa tcctgtccct ctagctcta 780
aaactttaca ccctcaagag gcttgaagag aaggagagg acctgaataa ggcgatggaa 840
agcgtggaa taaagaacaa ctttctcaag atgaagttca aatcttactt aaaggcaaac 900
tctaaagagg acttgaagaa cctaattcctc tccctccaga ggatagacgc tttttctaaa 960
ctttactttc aggacacagt gcagttgctg gggatttctt gacctcaaga ctggagaggg 1020
aagttgtgaa aaatacttct catggtgat aatctttttt atgaagtttgcgt 1080
tttcccggt tct 1093

<210> 124

<211> 350

<212> PRT

<213> Aquifex aeolicus

<400> 124

Val Glu Thr Thr Ile Phe Gln Phe Gln Lys Thr Phe Phe Thr Lys Pro
1 5 10 15

Pro Lys Glu Arg Val Phe Val Leu His Gly Glu Glu Gln Tyr Leu Ile
20 25 30

Arg Thr Phe Leu Ser Lys Leu Lys Glu Lys Tyr Gly Glu Asn Tyr Thr
35 40 45

Val Leu Trp Gly Asp Glu Ile Ser Glu Glu Glu Phe Tyr Thr Ala Leu
50 55 60

Ser Glu Thr Ser Ile Phe Gly Gly Ser Lys Glu Lys Ala Val Val Ile
65 70 75 80

Tyr Asn Phe Gly Asp Phe Leu Lys Lys Leu Gly Arg Lys Lys Lys Glu
85 90 95

Lys Glu Arg Leu Ile Lys Val Leu Arg Asn Val Lys Ser Asn Tyr Val
100 105 110

Phe Ile Val Tyr Asp Ala Lys Leu Gln Lys Gln Glu Leu Ser Ser Glu
115 120 125

Pro Leu Lys Ser Val Ala Ser Phe Gly Gly Ile Val Val Ala Asn Arg
130 135 140

Leu Ser Lys Glu Arg Ile Lys Gln Leu Val Leu Lys Lys Phe Lys Glu
145 150 155 160

Lys Gly Ile Asn Val Glu Asn Asp Ala Leu Glu Tyr Leu Leu Gln Leu
165 170 175

Thr Gly Tyr Asn Leu Met Glu Leu Lys Leu Glu Val Glu Lys Leu Ile
180 185 190

Asp Tyr Ala Ser Glu Lys Lys Ile Leu Thr Leu Asp Glu Val Lys Arg
195 200 205

Val Ala Phe Ser Val Ser Glu Asn Val Asn Val Phe Glu Phe Val Asp
210 215 220

Leu Leu Leu Lys Asp Tyr Glu Lys Ala Leu Lys Val Leu Asp Ser
225 230 235 240

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
245 250 255

Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
260 265 270

Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
275 280 285

Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
290 295 300

Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
305 310 315 320

Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
325 330 335

Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
340 345 350

<210> 125

<211> 1051

<212> DNA

<213> Aquifex aeolicus

<400> 125

atggaaaaag ttttttttga aaaactccag aaaaccttgc acatacccg aggactcctt 60
tttacggca aagaaggaag cgaaaaagacg aaaacagctt ttgaatttgc aaaaggatt 120
ttatgttaagg aaaacgtacc tggggatgcg gaagttgtcc ctccctgcaaa cacgtaaacg 180
agctggagga agcttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
cggtaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300
gagcggacat tacataaaga tagaacagat aagggaaagt aagaactttg cctatgtcaa 360
gcccgacta agcaggagaa aagtaattat aatagacgac gccccacgcga tgacctctca 420
ggcggcaaac gctctttaa agttatttga agagccacct gcggacacca cctttatctt 480
gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaactt ttcaagtgg 540
gttcaagggc ttttcagtaa aagaggttat ggaaatagcg aaagtagacg agggaaatagc 600
gaaactctct ggagggcagtc taaaaagggc tatcttacta aaggaaaaca aagatatcct 660
aaacaaagta aaggaattct tggaaaacga gccgtaaaaa gtttacaagc ttgcaagtga 720
attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattgg 780
atctcaaaaa ttgaccgaag agaaaaaaaga caattacacc taccttctt atacgatcag 840
actcttaaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
cgttcaggcg gattaataaa ccgttattga ttccgtaaaca tttaaacctt aatctaaatt 960
atgagagcct ttgaaggagg tctggtatgg aaaattgaa gattagatat atagatacga 1020
ggaagatagg aaccgtgagc ggtgtaaaag t 1051

<210> 126
<211> 305
<212> PRT
<213> Aquifex aeolicus

<400> 126

Met	Glu	Lys	Val	Phe	Leu	Glu	Lys	Leu	Gln	Lys	Thr	Leu	His	Ile	Pro
1				5				10						15	

Gly Gly Leu Leu Phe Tyr Gly Lys Glu Gly Ser Gly Lys Thr Lys Thr

20					25					30					
----	--	--	--	--	----	--	--	--	--	----	--	--	--	--	--

Ala Phe Glu Phe Ala Lys Gly Ile Leu Cys Lys Glu Asn Val Pro Trp

35				40					45						
----	--	--	--	----	--	--	--	--	----	--	--	--	--	--	--

Gly Cys Gly Ser Cys Pro Ser Cys Lys His Val Asn Glu Leu Glu Glu

50				55				60							
----	--	--	--	----	--	--	--	----	--	--	--	--	--	--	--

Ala Phe Phe Lys Gly Glu Ile Glu Asp Phe Lys Val Tyr Lys Asp Lys

65				70			75			80					
----	--	--	--	----	--	--	----	--	--	----	--	--	--	--	--

Asp Gly Lys Lys His Phe Val Tyr Leu Met Gly Glu His Pro Asp Phe

85				90				95							
----	--	--	--	----	--	--	--	----	--	--	--	--	--	--	--

Val Val Ile Ile Pro Ser Gly His Tyr Ile Lys Ile Glu Gln Ile Arg

100				105				110							
-----	--	--	--	-----	--	--	--	-----	--	--	--	--	--	--	--

Glu Val Lys Asn Phe Ala Tyr Val Lys Pro Ala Leu Ser Arg Arg Lys

115				120			125								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Val Ile Ile Ile Asp Asp Ala His Ala Met Thr Ser Gln Ala Ala Asn

130				135			140								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Ala Leu Leu Lys Val Leu Glu Glu Pro Pro Ala Asp Thr Thr Phe Ile

145				150			155			160					
-----	--	--	--	-----	--	--	-----	--	--	-----	--	--	--	--	--

Leu Thr Thr Asn Arg Arg Ser Ala Ile Leu Pro Thr Ile Leu Ser Arg

165				170			175								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Thr Phe Gln Val Glu Phe Lys Gly Phe Ser Val Lys Glu Val Met Glu

180				185			190								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Ile Ala Lys Val Asp Glu Glu Ile Ala Lys Leu Ser Gly Gly Ser Leu

195				200			205								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Lys Arg Ala Ile Leu Leu Lys Glu Asn Lys Asp Ile Leu Asn Lys Val

210				215			220								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile
245 250 255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
260 265 270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
275 280 285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
290 295 300

Asp
305

<210> 127

<211> 630

<212> DNA

<213> Aquifex aeolicus

<400> 127

atgaacttcc tgaaaaagtt ccttttactg agaaaaagctc aaaagtctcc ttacttcgaa 60
gaggttctacg aagaaaatcga tttgaaccag aaggtgaaag atgcaagggtt tgttagtttt 120
gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tccttcaat aggtgcgggt 180
gaggttaaaa acctgaaaat agacctctct aaatctttt acgagatact caaaaagtgcac 240
gagataaagg cggcggagat acatgaaata accagggaaag acgttgaaaa gtacggaaag 300
gaaccaaagg aagtaatata cgactttctg aagtacataa agggaaagcgt tctcggtggc 360
tactacgtga agtttgcgtt ctcactcggt gagaagttact ccataaagta cttccagtat 420
ccaatcatca actacaagtt agacctgttt agttcgtga agagagagta ccagagtggc 480
aggagtcttg acgacacctat gaagggaaactc ggtgtagaaa taagggcaag gcacaacgcc 540
cttgaagatg cctacataaac cgctcttctt ttccctaaagt acgtttaccc gaacagggag 600
tacagactaa aggtatccc gatttcctt 630

<210> 128

<211> 210

<212> PRT

<213> Aquifex aeolicus

<400> 128

Met Asn Phe Leu Lys Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser
1 5 10 15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

20

25

30

Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp
35 40 45

Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn
50 55 60

Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp
65 70 75 80

Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu
85 90 95

Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr
100 105 110

Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser
115 120 125

Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn
130 135 140

Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly
145 150 155 160

Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala
165 170 175

Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu
180 185 190

Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile
195 200 205

Phe Leu
210

<210> 129

<211> 526

<212> DNA

<213> Aquifex aeolicus

<400> 129

atgctcaata aggttttat aataggaaga cttacgggtg accccgttat aacttatcta 60
ccgagcggaa cgccccgtagt agagtttact ctggcttaca acagaaggta taaaaaccag 120
aacggtaat ttccaggagga aagtcaacttc tttgacgtaa aggcgtacgg aaaaatggct 180

gaagactggg ctacacgctt ctcgaaagga tacctcgta tcgttagaggg aagactctcc 240
caggaaaagt gggagaaaaga agaaaaagaag ttctcaaagg tcaggataat agcggaaaac 300
gtaagattaa taaacaggcc gaaagggtgct gaacttcaag cagaagaaga ggaggaagtt 360
cctcccattg aggagggaaat taaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataccctt ttaatttga ggaggttaaa gtatggtagt gagagctcct 480
aagaagaaaag ttgttatgta ctgtgaacaa aagagagac cagatt 526

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
1 5 10 15

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
20 25 30

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
35 40 45

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
50 55 60

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
65 70 75 80

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
85 90 95

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
100 105 110

Gln Ala Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
115 120 125

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
130 135 140

Ile Pro Phe

145

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

atgcaatttg tggataaaact tccctgtgac gaatccgcgg agagggcggt tcttggcagt 60
atgcttgaag acccccggaaa catacctctg gtacttgaat accttaaaga agaagacttc 120
tgcatacgacg agcacaagct acttttcagg gttcttacaa acctctggtc cgagtagcgc 180
aataagctcg atttcgatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240
atacctatag actggctcga agaactctac gaggaggcgg tatcccctga cacgcttgag 300
gaagtctgca aaatagtaaa acaaacgttcc gcacagaggg cgataattca actcggtata 360
gaactcattc acaaaggaaa ggaaaacaaa gactttcaca cattaatcga ggaagcccag 420
agcaggatat ttccatagc gggaaagtgc acatctacgc agttttacca tgtgaaagac 480
gttgcggaaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcggttcac ggaactcgat ctaaagacga cgggattcca ccctggagac 600
ttaataatac tcgcccgaag acccggtatg gggaaaaccg cctttatgct ctccataatc 660
tacaatctcg caaaaagacga gggaaaaccc tcagctgtat ttcccttgaa aatgagcaag 720
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tcttggaaagta tatacgaaatga agatttaaag aagcttgaag caagcgcaat agaactcgca 840
aagtagcaca tatacctcgca cgacacaccc gctctcacta caacggattt aaggataagg 900
gcaagaaagc tcagaaagga aaaggaagtt gagttcgtgg cggggacta cttgcaactt 960
ctgagaccgc cagtcggaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
ttaaaagccc ttgcaaaagga acttcacatt cccgttatgg cacttgcgca gctctccgt 1080
gaggtggaaa agaggagtga taaaagaccc cagctgcgg acctcagaga atccggacag 1140
atagaacagg acgcagacctt aatccctttc ctccacagac ccgagacta caagaaaaag 1200
ccaaatcccg aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260
acggacattt tgaagctcgc atttattaaag gagtacacta agtttgcaaa cctagaagcc 1320
cttccctgaac aacctcctga agaagaggaa ctttccggaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaaa ttaaggtttt ataattttt cttggctatc 1440
cgggtagct caatcggcag agcgggtggc tg 1472

<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
1 5 10 15

Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
20 25 30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
35 40 45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
50 55 60

Phe Val Leu Ile Lys Asp His Leu Glu Lys Lys Asn Leu Leu Gln Lys
65 70 75 80

Ile Pro Ile Asp Trp Leu Glu Glu Leu Tyr Glu Glu Ala Val Ser Pro
85 90 95

Asp Thr Leu Glu Glu Val Cys Lys Ile Val Lys Gln Arg Ser Ala Gln
100 105 110

Arg Ala Ile Ile Gln Leu Gly Ile Thr Ser Thr Gln Phe Tyr His Val
115 120 125

Lys Asp Val Ala Glu Glu Val Ile Glu Leu Ile Tyr Lys Phe Lys Ser
130 135 140

Ser Asp Arg Leu Val Thr Gly Leu Pro Ser Gly Phe Thr Glu Leu Asp
145 150 155 160

Leu Lys Thr Thr Gly Phe His Pro Gly Asp Leu Ile Ile Leu Ala Ala
165 170 175

Arg Pro Gly Met Gly Lys Thr Ala Phe Met Leu Ser Ile Ile Tyr Asn
180 185 190

Leu Ala Lys Asp Glu Gly Lys Pro Ser Ala Val Phe Ser Leu Glu Met
195 200 205

Ser Lys Glu Gln Leu Val Met Arg Leu Leu Ser Met Met Ser Glu Val
210 215 220

Pro Leu Phe Lys Ile Arg Ser Gly Ser Ile Ser Asn Glu Asp Leu Lys
225 230 235 240

Lys Leu Glu Ala Ser Ala Ile Glu Leu Ala Lys Tyr Asp Ile Tyr Leu
245 250 255

Asp Asp Thr Pro Ala Leu Thr Thr Asp Leu Arg Ile Arg Ala Arg
260 265 270

Lys Leu Arg Lys Glu Lys Glu Val Glu Phe Val Ala Val Asp Tyr Leu
275 280 285

Gln Leu Leu Arg Pro Pro Val Arg Lys Ser Ser Arg Gln Glu Glu Val
290 295 300

Ala Glu Val Ser Arg Asn Leu Lys Ala Leu Ala Lys Glu Leu His Ile
305 310 315 320

Pro	Val	Met	Ala	Leu	Ala	Gln	Leu	Ser	Arg	Glu	Val	Glu	Lys	Arg	Ser
		325						330						335	
Asp	Lys	Arg	Pro	Gln	Leu	Ala	Asp	Leu	Arg	Glu	Ser	Gly	Gln	Ile	Glu
	340						345							350	
Gln	Asp	Ala	Asp	Leu	Ile	Leu	Phe	Leu	His	Arg	Pro	Glu	Tyr	Tyr	Lys
	355					360							365		
Lys	Lys	Pro	Asn	Pro	Glu	Glu	Gln	Gly	Ile	Ala	Glu	Val	Ile	Ile	Ala
	370				375						380				
Lys	Gln	Arg	Gln	Gly	Pro	Thr	Asp	Ile	Val	Lys	Leu	Ala	Phe	Ile	Lys
	385				390				395					400	
Glu	Tyr	Thr	Lys	Phe	Ala	Asn	Leu	Glu	Ala	Leu	Pro	Glu	Gln	Pro	Pro
		405						410					415		
Glu	Glu	Glu	Leu	Ser	Glu	Ile	Ile	Glu	Thr	Gln	Glu	Asp	Glu	Gly	
		420					425						430		
Phe	Glu	Asp	Ile	Asp	Phe										
		435													

<210> 133
<211> 1526
<212> DNA
<213> Aquifex aeolicus

<400> 133
atgcctcggtacatagacgacttagacgg gaaatagata tagtagacgt catttccgaa 60
tacttaacttagagaaggtagttccaat tacagaacga actgtcccttcacccctgac 120
gatacaccctcctttacgtgtctccaagt aaacaaatat tcaagtgtttcggtgcggg 180
gtagggggagacgcgataaa gtcgtttccctttacgagg acatctccata ttgtgaagcc 240
gcccttgaacctcgcaaaaacgctacggaaagaaatttagacc ttgaaaagat atcaaaagac 300
gaaaaaggat acgtggctcttgacagggtttgtgatttctacaggaaacgatccttcaaa 360
aacagagaggcaagttagtgcgtaaagataggaaatagaccctaaatgcgaggaag 420
tttgatcttgcgttacgttgcactcgtaaaagtctttaaaagagaacgtatccttcaaa 480
cttttagaggcttaccttga aactaaaaacctccttctcctacgaagggtgtttacagg 540
gatcttttccttcgtgtgtcgatcccgataaaggatc cgaggggaaag agttataagg 600
ttcgggtggaa ggaggatagt agaggacaaa tctccaaatgcataaaactctccagac 660
agggtatttaaaaaggggagaacttattc ggtcttacgttgcggaaatggatataaag 720
gaagaaggat ttgcgtacttgtggaaagggtactttgacc ttgtttttccgag 780
ggaataagga acgttggcgttgc acccctcggttacgcccataatca ggcaaaacctc 840
ctttccaagt tcacaaaaaa ggtctacatccttacgacgttgcggatgtgcggaaatgg 900
gctatggaaa gtgccattccctactcctcagtgcaggatggaaatgttacccgtttac 960
ctccccgaag gatacgatcccgacgatgtttataaaggat tccggaaagaatggatataaaga 1020

agactgataa acagctcagg ggagctctt gaaacgctca taaaaaccgc aaggaaaac 1080
ttaggaga aaacgcgtga gttcaggtat tatctggct ttatccoga tggagtaagg 1140
cgcttgctc tggcttcgga gttcacacc aagtacaag ttcctatgga aattttatta 1200
atgaaaattg aaaaaaattc tcaagaaaaa gaaattaaac ttcctttaa ggaaaaaatc 1260
ttcctgaaag gactgataga attaaaacca aaaatagacc ttgaagtccct gaacttaagt 1320
cctgagttaa aggaactcgc agttaacgccc ttAAACGGAG aggagcatTT acTTCCAAA 1380
gaagttctcg agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440
ttacaaaaat ctggaaaaa gaggaagaaa agagggttga aaaatgtaaa tacttaatta 1500
actttaataa attttagag ttagga 1526

<210> 1:34
<211> 498
<212> PRT
<213> Aquifex aeolicus

<400> 134
Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
1 5 10 15

Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
20 25 30

Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
35 40 45

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
50 55 60

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
65 70 75 80

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
85 90 95

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
100 105 110

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
115 120 125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
130 135 140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
145 150 155 160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

165	170	175
Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys		
180	185	190
Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu		
195	200	205
Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys		
210	215	220
Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys		
225	230	235
Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg		
245	250	255
Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala		
260	265	270
Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val		
275	280	285
Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser		
290	295	300
Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr		
305	310	315
Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys		
325	330	335
Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr		
340	345	350
Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe		
355	360	365
Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu		
370	375	380
Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu		
385	390	395
Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe		
405	410	415
Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile		

420	425	430
Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val		
435	440	445
Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu		
450	455	460
Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp		
465	470	480
Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val		
485	490	495

Asn Thr

<210> 135
<211> 705
<212> DNA
<213> Aquifex aeolicus

<400> 135
atgcaagata ccgctacctg cagtatttgc caggggacgg gattcgtaaa gaccgaagac 60
aacaaggtaa ggctctgcga atgcagggttc aagaaaaggg atgtaaacag ggaactaaac 120
atcccaaaga ggtactggaa cgccaaactta gacacttacc accccaagaa cgtatcccag 180
aacagggcac ttttgacgat aagggtcttc gtccacaact tcaatcccgaa ggaagggaaa 240
gggcttacct ttgttaggatc tcctggagtc ggcaaaaactc accttgcgggt tgcaacatta 300
aaagcgattt atgagaagaa ggaatcaga ggataacttct tcgatacgaa ggatctaata 360
ttcaggttaa aacacttaat ggacgaggaa aaggatacaa agtttttaaa aactgtctta 420
aactcaccgg ttttgggtct cgacgacctc ggttctgaga ggctcagtgaa ctggcagagg 480
gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540
acgaattact cactccagag ggaagaagag agtagcgtga ggataagtgc ggatcttgca 600
agcagactcg gagaaaacgt agtttcaaaa atttacgaga tgaacgagtt gctcggtata 660
aagggttccg acctcaggaa gtctaaaaag ctatcaaccc catct 705

<210> 136
<211> 235
<212> PRT
<213> Aquifex aeolicus

<400> 136
Met Gln Asp Thr Ala Thr Cys Ser Ile Cys Gln Gly Thr Gly Phe Val
1 5 10 15
Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys

20

25

30

Arg Asp Val Asn Arg Glu Leu Asn Ile Pro Lys Arg Tyr Trp Asn Ala
35 40 45

Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu
50 55 60

Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys
65 70 75 80

Gly Leu Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala
85 90 95

Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr
100 105 110

Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp
115 120 125

Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val
130 135 140

Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg
145 150 155 160

Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser
165 170 175

Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Ser Ser
180 185 190

Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val
195 200 205

Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp
210 215 220

Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser
225 230 235

<210> 137

<211> 4101

<212> DNA

<213> Thermatoga maritima

<400> 137

ataaaaaaa ttgaaaattt gaagtggaaa aatgtctcg ttaaaagcct gaaaatagat 60
ccgatgcag gtgtggttct cgttccgtg gaaaaattct ccgaagagat agaagacctt 120
gtcggttac tggagaagaa gacgcggtt cgagtcatcg tgaacggtgt tcaaaaaagt 180
aacggggatc taagggaaa gatacttcc ctctcaacg gtaatgtgcc ttacataaaa 240
gatgttgtt tcgaaggaaa caggctgatt ctgaaagtgc ttggagattt cgcgccggac 300
aggatgcct ccaaactcag aagcacgaaa aaacagctcg atgaactgct gcctccgga 360
acagagatca tgctggaggt tgtggagctt ccggaagatc ttttggaaaa ggaagtacca 420
caaccagaaa agagagaaga accaaagggt gaagaattga agatcgagga tgaaaaccac 480
atcttggac agaaacccag aaagatcgtc ttcacccctt caaaaatctt tgagtacaac 540
aaaaagacat cggtaaggg caagatcttca aaaatagaga agatcgaggg gaaaagaacg 600
gtcctctga ttacactgac agacggagaa gattctctga tctgcaaagt ctcaacgac 660
gttggaaaagg tcgaaggaa agtatcggtt ggagacgtga tcgttgccac aggagacctc 720
cttctgaaa acggggagcc caccctttac gtgaaggaa tcacaaaact tccccaagcg 780
aaaaggatgg acaaacttcc ggttaagagg gtggagctcc acgcccatac caagttcagc 840
gatcaggacg caataacaga tgtgaacgaa tatgtgaaac gagccaagga atggggcttt 900
cccgcatcg ccctcacgga tcatggaaac gttcaggcca taccttactt ctacgacgac 960
gcgaaagaag ctggaataaaa gcccattttgc ggtatcgaaag cgtatctggt gagtgacgtg 1020
gagccgtca taaggaatct ctccgacgat tcgacgttgc gagatgccac gttcgtcg 1080
ctcgacttcg agacgacggg ttcgaccccg caggtggatg agatcatcgat gataggagcg 1140
gtgaagatac agggtggcca gatagtggac ggttaccaca ctctcataaa gccttccagg 1200
gagatctcaa gaaaaagtttgc ggttaccacc ggaatcactc aagagatgtt gggaaaacaag 1260
agaagcatcg aggaaggatcttgc ggttaccacc ttcggttttc tggaagatccatcatcgta 1320
gcacacaacg ccaacttcgatc ctacagattt ctgaggctgtt ggttccatggatgg 1380
tttgacttggg aaagacccta catagatacg ctgccttcg caaatccctt tctcaaactg 1440
agaagctact ctctggatttgc ggttaccacc ttcggttttc tggttccatggatgg 1500
aggccctgg atgacgacggg ggttccatggatgg 1560
aagaagatcg gtatcagaa gcttccatggatgg 1620
accgcgttca aacccttccatggatgg 1680
ctatacaac tggtttctga ttccatggatgg 1740
aaaagtggatcg tcatcgatc ggttccatggatgg 1800
gagatcgatcg gttccatggatgg 1860
tttctcgact acatagaatcg tcatcgatcg ggttccatggatgg 1920
gacagagaaa gactgaaatcg gttccatggatgg 1980
aagttcgatcg tcatcgatcg ggttccatggatgg 2040
gctgcacttc tggcacccatggatgg 2100
agaacgaccg aagaatcgatcg ggttccatggatgg 2160
agggaaatcg tcatcgatcg ggttccatggatgg 2220
ctcgatcgatcg aacttcacccatggatgg 2280
accatcgatcg gggcgatcgatcg ggttccatggatgg 2340
gtgaaaagg aactcgatcgatcg ggttccatggatgg 2400
caggatcgatcg ttcagaaatcgatcg ggttccatggatgg 2460
gggtccatggatgg 2520
tacaggatcgatcg cagatcgatcg ggttccatggatgg 2580
tacgacccatggatgg 2640
ggcataccatggatgg 2700
aacttcctcgatcg ggttccatggatgg 2760
gaccacgtct atagggcg 2820
gtgagaagatcgatcg aaccatcgatcg ggttccatggatgg 2880

gttccatga tcacggagt gaagagaacg acgggtcagc acccaggggg gctcatgatc 2940
 ataccgaaag acaaagaagt ctacgatttc actcccatac agtatccagc caacgataga 3000
 aacgcaggtg tgttcaccac gcacttcgca tacgagacga tccatgatga cctggtgaag 3060
 atagatgcgc tcggccacga tcatcccact ttcatcaaga tgctcaagga cctcaccgga 3120
 atcgatccca tgacgattcc catggatgac cccgatacgc tcgccatatt cagttctgtg 3180
 aagcctcttg gtgtggatcc cgtttagtgc gaaagcgatg tggaaacgta cggaattccg 3240
 gagttcgaa ccgagttgt gaggggaaatg ctcgtgaaa cgagacaaa gagttcgcc 3300
 gagttgtga gaatctcagg actgtcacac ggtacggacg tctggttgaa caacgcacgt 3360
 gattggataa acctcgcta cgccaagctc tccgaggtt ttcgtgtag ggacgacatc 3420
 atgaacttcc tcatacacaa aggaatggaa ccgtcacttg cttcaagat catggaaaac 3480
 gtcaggaagg gaaagggtat cacagaagag atggagagcg agatgagaag gctgaagggtt 3540
 ccagaatggt tcatacgatc ctgtaaaagg atcaaataatc tcttccgaa agtcacgct 3600
 gtggcttacg tgagtatggc cttcagaatt gcttacttca aggttacta tcctcttcag 3660
 tttacgcgg cgtacttcac gataaaaggat gatcagttcg atccggttct cgtactcagg 3720
 ggaaaagaag ccataaagag gcgcttgaga gaactcaaag cgatgcctgc caaagacgcc 3780
 cagaagaaaa acgaagttag tttctggag gttccctgg aaatgataact gagaggttt 3840
 tccttcctac cgccccacat cttcaaatcc gacgcgaaga aatttctgtat agaaggaaac 3900
 tcgctgagaa ttccgttcaa caaacttcca ggactgggtg acagcgttgc cgagtcgata 3960
 atcagagcca gggaaagaaaa gcgcgttcaact tcggttggaaatctcatgaa gaggaccaag 4020
 gtcaacaaaaa atcacataga gctgatgaaa agcctgggtg ttctcgggaa ccttccagag 4080
 acgaaacagt tcacgctttt c 4101

<210> 138
 <211> 1367
 <212> PRT
 <213> Thermatoga maritima

<400>	138															
Met	Lys	Lys	Ile	Glu	Asn	Leu	Lys	Trp	Lys	Asn	Val	Ser	Phe	Lys	Ser	
1																15
Leu	Glu	Ile	Asp	Pro	Asp	Ala	Gly	Val	Val	Leu	Val	Ser	Val	Glu	Lys	
																30
Phe	Ser	Glu	Glu	Ile	Glu	Asp	Leu	Val	Arg	Leu	Leu	Glu	Lys	Lys	Thr	
																45
Arg	Phe	Arg	Val	Ile	Val	Asn	Gly	Val	Gln	Lys	Ser	Asn	Gly	Asp	Leu	
																50
Arg	Gly	Lys	Ile	Leu	Ser	Leu	Leu	Asn	Gly	Asn	Val	Pro	Tyr	Ile	Lys	
																65
Asp	Val	Val	Phe	Glu	Gly	Asn	Arg	Leu	Ile	Leu	Lys	Val	Leu	Gly	Asp	
																85
Phe	Ala	Arg	Asp	Arg	Ile	Ala	Ser	Lys	Leu	Arg	Ser	Thr	Lys	Lys	Gln	

100	105	110
Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val		
115	120	125
Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys		
130	135	140
Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His		
145	150	155
Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile		
165	170	175
Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile		
180	185	190
Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp		
195	200	205
Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val		
210	215	220
Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu		
225	230	240
Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys		
245	250	255
Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu		
260	265	270
Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val		
275	280	285
Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala		
290	295	300
Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala		
305	310	320
Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu		
325	330	335
Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr		
340	345	350
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu		

355	360	365
Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln		
370	375	380
Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg		
385	390	395
400		
Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met		
405	410	415
Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly		
420	425	430
Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr		
435	440	445
Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu		
450	455	460
Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu		
465	470	475
480		
Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro		
485	490	495
Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val		
500	505	510
Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu		
515	520	525
Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys		
530	535	540
Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn		
545	550	555
560		
Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val		
565	570	575
Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu		
580	585	590
Val Gly Ser Ala Cys Ile Ser Gly Glu Leu Gly Arg Ala Ala Leu Glu		
595	600	605
Gly Ala Ser Asp Ser Glu Leu Glu Ile Ala Lys Phe Tyr Asp Tyr		

610	615	620
Ile Glu Val Met Pro Leu Asp Val Ile Ala Glu Asp Glu Glu Asp Leu		
625	630	635
Asp Arg Glu Arg Leu Lys Glu Val Tyr Arg Lys Leu Tyr Arg Ile Ala		
645	650	655
Lys Lys Leu Asn Lys Phe Val Val Met Thr Gly Asp Val His Phe Leu		
660	665	670
Asp Pro Glu Asp Ala Arg Gly Arg Ala Ala Leu Leu Ala Pro Gln Gly		
675	680	685
Asn Arg Asn Phe Glu Asn Gln Pro Ala Leu Tyr Leu Arg Thr Thr Glu		
690	695	700
Glu Met Leu Glu Lys Ala Ile Glu Ile Phe Glu Asp Glu Glu Ile Ala		
705	710	715
Arg Glu Val Val Ile Glu Asn Pro Asn Arg Ile Ala Asp Met Ile Glu		
725	730	735
Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn		
740	745	750
Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile		
755	760	765
Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu		
770	775	780
Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala		
785	790	795
Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser		
805	810	815
Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr		
820	825	830
Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr		
835	840	845
Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro		
850	855	860
Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His		

865	870	875	880
Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro			
885	890	895	
Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg			
900	905	910	
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr			
915	920	925	
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr			
930	935	940	
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu			
945	950	955	960
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly			
965	970	975	
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro			
980	985	990	
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His			
995	1000	1005	
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu			
1010	1015	1020	
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly			
1025	1030	1035	1040
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile			
1045	1050	1055	
Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser			
1060	1065	1070	
Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg			
1075	1080	1085	
Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg			
1090	1095	1100	
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg			
1105	1110	1115	1120
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys			

1125	1130	1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser		
1140	1145	1150
Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr		
1155	1160	1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe		
1170	1175	1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala		
1185	1190	1195
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His		
1205	1210	1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln		
1220	1225	1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg		
1235	1240	1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn		
1250	1255	1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe		
1265	1270	1275
Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu		
1285	1290	1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu		
1300	1305	1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro		
1315	1320	1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn		
1330	1335	1340
His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu		
1345	1350	1355
Thr Glu Gln Phe Thr Leu Phe		
1365		

<210> 139
<211> 567
<212> DNA
<213> Thermatoga maritima

<400> 139
gtgctgccca tgatatggaa cgacaccgtt tttgcgtcg tagacacaga aaccacggga 60
accgatccct ttgccggaga ccggatagtt gaaatacgcc ctgttcctgt cttcaagggg 120
aagatctaca gaaacaaagc gtttcactct ctcgtgaatc ccagaataag aatccctgcg 180
ctgattcaga aagttcacgg ttcgtcaac atggacatcg tggaaacgg tgctcgtgt tcacaacgcc 240
acagttacg atctttcag ggattacgtg aagggaaacgg tgctcgtgt tcacaacgcc 300
aacttcgacc tcactttct ggatatgtat gcaaaggaaa cgggaaactt tccaataacg 360
aatccctaca tcgacacact cgatcttca gaagagatct ttggaaaggcc tcattcttc 420
aaatggctct ccgaaagact tggaaataaaa accacgatac ggcaccgtgc tcttccagat 480
gccctggta ccgcaagagt tttgtgaag cttgtgaat ttcttggtga aaacagggtc 540
aacgaattca tacgtggaaa acgggggg 567

<210> 140
<211> 189
<212> PRT
<213> Thermatoga maritima

<400> 140
Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr
1 5 10 15

Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
20 25 30

Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
35 40 45

His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
50 55 60

Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
65 70 75 80

Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
85 90 95

Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
100 105 110

Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
115 120 125

```

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
130                      135                      140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
145                      150                      155                      160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
165                      170                      175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
180                      185

```

<210> 141
<211> 1434
<212> DNA
<213> *Thermatoga maritima*

<400> 141
gtggaatgttcc ttacaggaa gtacaggcca aagactttt ctgaggttgt caatcaggat 60
catgtgaaga aggcaataat cggtgttatt cagaagaaca gcgtggccca cggatacata 120
ttcgccgtc cgagggaaac gggaaagact actcttgcca gaattctcgc aaaatccctg 180
aactgtgaga acagaaaagg agttgaaccc tgcaattcct gcagagcctg cagagagata 240
gacgaggaa ccttcatttga cgtgatagag ctcgacgcgg cctccaacag aggaatagac 300
gagatcagaa gaatcagaga cgcgttgg tacaggccga tggaaaggta atacaagtc 360
tacataatag acgaagttca catgctcacg aaagaaggct tcaacgcgct cctcaaaaca 420
ctcgaagaac ctcccttccc cgtcggttgc gtgctggcaa cgacaaaacct tgagaagggt 480
cctcccacga ttatctcgag atgtcagggtt ttcgagttca gaaacattcc cgacgagctc 540
atcgaaaaga ggctccagga agttcgagg gctgaaggaa tagagataga caggaaagct 600
ctgagcttca tcgcaaaaag agcctcttga ggcttggag acgcgcac tcaatcgag 660
caggtgttgg agttctcgga aggaaagata gatctcgaga cggatcacag ggcgctcggg 720
ttgataccga tacagggttgc tcgcgattac gtgaacgcta tctttctgg tgatgtgaaa 780
agggtcttca ccgttctcgta cgacgtctat tacagcggga aggactacga ggtgctcatt 840
caggaagcag tcgaggatct ggtcgaagac ctggaaagg agagagggtt ttaccagggtt 900
tcagcgaacg atatagttca gtttcgaga caacttctga atttctgag agagataaaag 960
ttcgccgaag aaaaacgact cgtctgtaaa gtgggttcgg cttacatagc gacgagggttc 1020
tccaccacaa acgttcagga aaacgatgtc agagaaaaaa acgataattc aaatgtacag 1080
cagaaagaag agaagaaaaga aacggtgaag gcaaaagaag aaaaacagga agacagcgg 1140
ttcgagaaac gcttcaaaga actcatggaa gaactgaaaag aaaaggcga tctcttatac 1200
tttgcgttc tcagcctctc agaggtgcag tttgacggag aaaaggtgat tattttttt 1260
gattcatcgaa aagcttatgca ttacgagttt atgaagaaaa aactgcctga gctggaaaac 1320
atttttcttca gaaaactcgg gaaaaaaagtta gaagttgaac ttgcactgat gggaaaaagaa 1380
qaaacaatcq aqaagqtttc tcagaqatc ctqaqattgt ttqaacqqa qqqq 1434

<210> 142
<211> 478
<212> PRT

<213> Thermatoga maritima

<400> 142

Met Glu Val Leu Tyr Arg Lys Tyr Arg Pro Lys Thr Phe Ser Glu Val
1 5 10 15

Val Asn Gln Asp His Val Lys Lys Ala Ile Ile Gly Ala Ile Gln Lys
20 25 30

Asn Ser Val Ala His Gly Tyr Ile Phe Ala Gly Pro Arg Gly Thr Gly
35 40 45

Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ser Leu Asn Cys Glu Asn
50 55 60

Arg Lys Gly Val Glu Pro Cys Asn Ser Cys Arg Ala Cys Arg Glu Ile
65 70 75 80

Asp Glu Gly Thr Phe Met Asp Val Ile Glu Leu Asp Ala Ala Ser Asn
85 90 95

Arg Gly Ile Asp Glu Ile Arg Arg Ile Arg Asp Ala Val Gly Tyr Arg
100 105 110

Pro Met Glu Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Val His Met
115 120 125

Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro
130 135 140

Pro Ser His Val Val Phe Val Leu Ala Thr Thr Asn Leu Glu Lys Val
145 150 155 160

Pro Pro Thr Ile Ile Ser Arg Cys Gln Val Phe Glu Phe Arg Asn Ile
165 170 175

Pro Asp Glu Leu Ile Glu Lys Arg Leu Gln Glu Val Ala Glu Ala Glu
180 185 190

Gly Ile Glu Ile Asp Arg Glu Ala Leu Ser Phe Ile Ala Lys Arg Ala
195 200 205

Ser Gly Gly Leu Arg Asp Ala Leu Thr Met Leu Glu Gln Val Trp Lys
210 215 220

Phe Ser Glu Gly Lys Ile Asp Leu Glu Thr Val His Arg Ala Leu Gly
225 230 235 240

Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser
245 250 255

Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser
260 265 270

Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val
275 280 285

Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp
290 295 300

Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys
305 310 315 320

Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile
325 330 335

Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu
340 345 350

Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr
355 360 365

Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg
370 375 380

Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile
385 390 395 400

Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val
405 410 415

Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys
420 425 430

Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys
435 440 445

Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu
450 455 460

Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly
465 470 475

<210> 143
<211> 1098

<212> DNA

<213> Thermatoga maritima

<400> 143

atgaaagtaa ccgtcacgac tcttgaattt aaagacaaaa taaccatcgc ctcaaaaagcg 60
ctcgcaaaga aatccgtgaa acccatttt gctggatttc ttttcgaagt gaaagatgga 120
aatttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacf ttttggta ccaggagatg tcattcagaa gatggtaag 240
gttctcccag atgagataac ggaactttct tttaggggg atgctctgt tataagttct 300
ggaagcaccg tttcaggat caccacatg cccgcggacg aatttccaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat ggtgaaaag 420
gtcatcttcg ccgctgccaa agacgagttc atgcgaaatc tgaatggagt tttctggaa 480
ctccacaaga atcttctcag gctggttgca agtgatggtt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaaacg tgctggacaa cacaacggag ccgactataa ccgtgaggtt ccatggaa 660
agggtttctc tgctgacaaa tgatgtagaa acgggtgatga gagtggtcga cgctgaattt 720
cccgattaca aaagggtgat ccccgaaact ttcaaaaacga aagtgggtt ttccagaaaa 780
gaactcaggg aatcttgcgaa gagggtgatg gtgattgcca gcaaggaaag cgagtccgtg 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagccccga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaagaa gggaaagatc tcgtgatcgc ttcaacccg 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaat gaaatcggtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggataacct ttacatagtg 1080
atgccccatca gactggca 1098

<210> 144

<211> 366

<212> PRT

<213> Thermatoga maritima

<400> 144

Met Lys Val Thr Val Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile

1

5

10

15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly

20

25

30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp

35

40

45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly

50

55

60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys

65

70

75

80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu

85

90

95

Val Ile Ser Ser Gly Ser Thr Val Phe Arg Ile Thr Thr Met Pro Ala
100 105 110

Asp Glu Phe Pro Glu Ile Thr Pro Ala Glu Ser Gly Ile Thr Phe Glu
115 120 125

Val Asp Thr Ser Leu Leu Glu Glu Met Val Glu Lys Val Ile Phe Ala
130 135 140

Ala Ala Lys Asp Glu Phe Met Arg Asn Leu Asn Gly Val Phe Trp Glu
145 150 155 160

Leu His Lys Asn Leu Leu Arg Leu Val Ala Ser Asp Gly Phe Arg Leu
165 170 175

Ala Leu Ala Glu Glu Gln Ile Glu Asn Glu Glu Glu Ala Ser Phe Leu
180 185 190

Leu Ser Leu Lys Ser Met Lys Glu Val Gln Asn Val Leu Asp Asn Thr
195 200 205

Thr Glu Pro Thr Ile Thr Val Arg Tyr Asp Gly Arg Arg Val Ser Leu
210 215 220

Ser Thr Asn Asp Val Glu Thr Val Met Arg Val Val Asp Ala Glu Phe
225 230 235 240

Pro Asp Tyr Lys Arg Val Ile Pro Glu Thr Phe Lys Thr Lys Val Val
245 250 255

Val Ser Arg Lys Glu Leu Arg Glu Ser Leu Lys Arg Val Met Val Ile
260 265 270

Ala Ser Lys Gly Ser Glu Ser Val Lys Phe Glu Ile Glu Glu Asn Val
275 280 285

Met Arg Leu Val Ser Lys Ser Pro Asp Tyr Gly Glu Val Val Asp Glu
290 295 300

Val Glu Val Gln Lys Glu Gly Glu Asp Leu Val Ile Ala Phe Asn Pro
305 310 315 320

Lys Phe Ile Glu Asp Val Leu Lys His Ile Glu Thr Glu Glu Ile Glu
325 330 335

Met Asn Phe Val Asp Ser Thr Ser Pro Cys Gln Ile Asn Pro Leu Asp
340 345 350

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
355 360 365

<210> 145
<211> 972
<212> DNA
<213> Thermatoga maritima

<400> 145

atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60
ctcctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
gatttcataa ggtctttact caggacaaag acgatcttt ccaacaagac gatcattgac 180
atcgtaatt tcgatgagtg gaaagcacag gagcagaagc gtctcggtga actttgaaa 240
aacgtaccgg aagacgttca tatcttcatc cgttctcaa aaacaggtgg aaaggagta 300
gcgcgtggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360
ttcagggaga atggtttgct catcgataaa gatgccctc agctgtttt ctccaagggtt 420
ggaacgaacg acctgatcat agaaagggag attgaaaaac tgaaagctta ttccgaggac 480
agaaagataa cggtagaaga cgtgaaagag gtcgtttta cctatcagac tccgggatac 540
gatgatTTTt gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600
cagctgtgga aaaccacaga gtccgtggg attgccactg tcctgcgaa tcacttctt 660
gatctcttca aaatcctcgt tcttgtaca aagaaaagat actacacctg gcctgatgtg 720
tccagggtgt ccaaagagct gggattccc gttccctcgtg tggctcggtt cctcggtttc 780
tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
gttagaaaga tactgagggta tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttcttccag 960
agagatgaag aa 972

<210> 146
<211> 324
<212> PRT
<213> Thermatoga maritima

<400> 146

Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
1 5 10 15

Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
20 25 30

His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
35 40 45

Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
50 55 60

Asp	Glu	Trp	Lys	Ala	Gln	Glu	Gln	Lys	Arg	Leu	Val	Glu	Leu	Leu	Lys
65						70						75			80
Asn	Val	Pro	Glu	Asp	Val	His	Ile	Phe	Ile	Arg	Ser	Gln	Lys	Thr	Gly
						85						90			95
Gly	Lys	Gly	Val	Ala	Leu	Glu	Leu	Pro	Lys	Pro	Trp	Glu	Thr	Asp	Lys
						100						105			110
Trp	Leu	Glu	Trp	Ile	Glu	Lys	Arg	Phe	Arg	Glu	Asn	Gly	Leu	Leu	Ile
						115						120			125
Asp	Lys	Asp	Ala	Leu	Gln	Leu	Phe	Phe	Ser	Lys	Val	Gly	Thr	Asn	Asp
						130						135			140
Leu	Ile	Ile	Glu	Arg	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Tyr	Ser	Glu	Asp
						145						150			160
Arg	Lys	Ile	Thr	Val	Glu	Asp	Val	Glu	Glu	Val	Val	Phe	Thr	Tyr	Gln
						165						170			175
Thr	Pro	Gly	Tyr	Asp	Asp	Phe	Cys	Phe	Ala	Val	Ser	Glu	Gly	Lys	Arg
						180						185			190
Lys	Leu	Ala	His	Ser	Leu	Leu	Ser	Gln	Leu	Trp	Lys	Thr	Thr	Glu	Ser
						195						200			205
Val	Val	Ile	Ala	Thr	Val	Leu	Ala	Asn	His	Phe	Leu	Asp	Leu	Phe	Lys
						210						215			220
Ile	Leu	Val	Leu	Val	Thr	Lys	Lys	Arg	Tyr	Tyr	Thr	Trp	Pro	Asp	Val
						225						230			240
Ser	Arg	Val	Ser	Lys	Glu	Leu	Gly	Ile	Pro	Val	Pro	Arg	Val	Ala	Arg
						245						250			255
Phe	Leu	Gly	Phe	Ser	Phe	Lys	Thr	Trp	Lys	Phe	Lys	Val	Met	Asn	His
						260						265			270
Leu	Leu	Tyr	Tyr	Asp	Val	Lys	Lys	Val	Arg	Lys	Ile	Leu	Arg	Asp	Leu
						275						280			285
Tyr	Asp	Leu	Asp	Arg	Ala	Val	Lys	Ser	Glu	Glu	Asp	Pro	Lys	Pro	Phe
						290						295			300
Phe	His	Glu	Phe	Ile	Glu	Glu	Val	Ala	Leu	Asp	Val	Tyr	Ser	Leu	Gln
						305						310			320

Arg Asp Glu Glu

<210> 147
<211> 936
<212> DNA
<213> Thermatoga maritima

<400> 147
atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60
gaaaaagtctg aaggaatatac catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgttctg 180
gagatagatc ccgaggggga gaacataggc atagacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
atgaccgc aggcggcgaa cgcggttctg aaggcccttg aagaaccacc agaatacgct 360
gtgatcggttc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttctttag agagacttca aaacggctct cgaagcctac 540
aaacttggtg cgaaaaaact ttctggattt atggaaagtc tcaaagttt ggagacggaa 600
aaactcttga aaaaggcct ttcaaaaaggc ctcgaagggtt atctcgcatg tagggagctc 660
ctggagagat tttcaaagggt ggaatcgaag gaattcttgc cgcttttga tcaggtgact 720
aacacgataa cagaaaaaga cgcggttctt ttgatccaga gactgacaag aatcattctc 780
cacaaaaaca catgggaaag cgttgaagat caaaaaagcg tgtcttcct cgattcaatt 840
ctcagggtga agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936

<210> 148
<211> 311
<212> PRT
<213> Thermatoga maritima

<400> 148
Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
1 5 10 15
Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
20 25 30
Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
35 40 45
Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
50 55 60
Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
65 70 75 80

Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His
85 90 95

Asp Cys Glu Arg Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala
100 105 110

Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg
115 120 125

Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val
130 135 140

Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly
145 150 155 160

Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala
165 170 175

Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu
180 185 190

Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser
195 200 205

Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe
210 215 220

Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr
225 230 235 240

Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr
245 250 255

Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Lys Ser
260 265 270

Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu Asn
275 280 285

Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg Lys
290 295 300

Arg Gly Val Asn Ala Trp Ser
305 310

<210> 149

<211> 423
<212> DNA
<213> Thermatoga maritima

<400> 149
atgtcttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60
tacacgctca gcggaaactcc agtcaccacc ttccacccatcg cggtggacag ggttcccaga 120
aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcgtcac ctggaaaga 180
ctggcagagt tcgctagaac ctatctcacc aaaggaaaggc tcgttctcggt cgaagggtgaa 240
atgagaatga gaagatggg aacacccact ggagaaaaga gggtatctcc ggaggttgtc 300
gcaaacgttg tttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
gagctggaaa taccggaaga agactttcc agcgataacct tcagtgaaga tgaaccacca 420
ttt 423

<210> 150
<211> 141
<212> PRT
<213> Thermatoga maritima

<400> 150
Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
1 5 10 15

Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Phe Thr
20 25 30

Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
35 40 45

Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
50 55 60

Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
65 70 75 80

Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
85 90 95

Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
100 105 110

Glu Thr Val Ser Glu Thr Glu Glu Leu Glu Ile Pro Glu Glu Asp
115 120 125

Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
130 135 140

<210> 151
<211> 1353
<212> DNA
<213> Thermatoga maritima

<400> 151
atgcgtgttc ccccgacaa cttagaggcc gaagttgctg tgctcggaa catattgata 60
gatccgtcgg taataaacga cgttcttcaa attttgagcc acgaagattt ctatctgaaa 120
aaacaccaac acatcttcag agcgatggaa gagcttacg acgaaggaaa accgggtggac 180
gtggttccg tctgtgacaa gcttcaaagc atggaaaac tcgaggaatg aggtggagat 240
ctgaaagtgg cccagctcgc tgaggctgtg cccagttctg cacacgcact tcactacgac 300
gagatgtca aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgatc 420
ttcgagatct cagagatgaa aacgacaaa tcctacgatc atctgagagg catcatgcac 480
cgggttttgg aaaacctgga gaacttcagg gaaagagcca accttataga accgggtgt 540
ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac agggttccac 600
agctccgatc tggtaataat agcagcgaga ccctccatgg gaaaaacctc cttcgactc 660
tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
atgtccaagg aacagctcgc tcaaagacta ctcagcatgg agtccgggtg ggatctttac 780
agcatcagaa caggataacct ggatcaggag aagtggaaa gactcacaat agcggcttct 840
aaactctaca aagcacccat agttgtggac gatgagtcac tcctcgatcc gcgatcggt 900
agggcaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccattt tgtcactat 960
ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020
tcgagatctc tgaagctcct tgcgaggaa ctcgacatag tggtgatagc gcttcacag 1080
cttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtgaa cctcaggaa 1140
tccgggtcga tagaacagga cgcagacaca gtcatctca tctacaggaa ggaatattac 1200
aggagcaaaa aatccaaaga gggaaagcaag cttcacgaac ctcacgaagc tggaaatcata 1260
ataggtaaac agagaaacgg tcccgttggaa acgatcactc tgatctcgaa ccccagaacg 1320
gttacgttcc atgaagtcga tgggtgcattca 1353

<210> 152
<211> 451
<212> PRT
<213> Thermatoga maritima

<400> 152
Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
1 5 10 15

Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
20 25 30

Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
35 40 45

Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val

50	55	60
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp		
65	70	75
Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala		
85	90	95
Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu		
100	105	110
Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp		
115	120	125
Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser		
130	135	140
Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His		
145	150	155
Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile		
165	170	175
Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu		
180	185	190
Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala		
195	200	205
Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg		
210	215	220
Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu		
225	230	235
Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly		
245	250	255
Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp		
260	265	270
Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val		
275	280	285
Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala		
290	295	300
Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr		

305	310	315	320
Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu			
325	330	335	
Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp			
340	345	350	
Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg			
355	360	365	
Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile			
370	375	380	
Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr			
385	390	395	400
Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu			
405	410	415	
Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile			
420	425	430	
Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val			
435	440	445	
Val His Ser			
450			

<210> 153
 <211> 1695
 <212> DNA
 <213> Thermatoga maritima

<400> 153
 gtgattcctc gagaggtcat cgaggaaata aaagaaaaagg ttgacatcg agaggtcatt 60
 tccgagtacg tgaatcttac cccggtaggt tcctcctaca gggctctctg tccctttcat 120
 tcagaaacca atccttcttt ctacgttcat ccgggtttga agatatacca ttgtttcggc 180
 tgcgggtcga gtggagacgt catcaaattt cttcaagaaa tggaaaggat cagtttccag 240
 gaagcgcgtgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaaa 300
 gggacttctg aatacgtaaa atacattcgat ttgtacgaag aaacgtggaa aaggtaacgtc 360
 aaagagctgg agaaatcgaa agaggcaaaa gactattaa aaagcagagg cttctctgaa 420
 gaagatatacg caaagttcgg ctttgggtac gtccccaga gatccagcat ctctatagaa 480
 gttgcagaag gcatgaacat aacactggaa gaacttgtca gatacggat cgcgctgaaa 540
 aagggtgatc gattcgttga tagattcgaa ggaagaatcg ttgttccaat aaagaacgac 600
 agtggtcata ttgtggctt tggtgccgt gctctggca acgaagaacc gaagtatttg 660
 aactctccag agaccaggtt aaaaaatccc tttttctttt cgtatggcg 720

aaaaaaagtgg caaaagaggt tggtttttc gtcacaccg aaggctactt cgacgcgc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaacttc ggcgtattcg aaaaacgtca tactgtgtt cgataatgac 900
aaagcaggct tcagagccac tctcaaattcc ctcgaggatc tccttagacta cgaattcaac 960
gtgcttgcgg 1020
caacccctc tccttacaaa gaccagatg aactcttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaac tcgcgttcgt tcgaatattt tctggtgacg 1080
gctggtgagg tcttcttga caggaacagc cccgcgggtg tgagatccta cctttcttc 1140
ctcaaagggtt gggtccaaaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtaatgagg tttcatcttc tctccagata ccagaaaaacc agatttgaa ctttttgaa 1260
agcgacaggt ctaacactat gcctgttcat gagaccaagt cgtcaaagggt ttacgatgag 1320
gggagaggac tggcttattt gttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaaac gcgagggagt tttcaagag agtctcactg 1440
ggagaagatt tgaacaaaagt catagaaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccggaa aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgcag aaatagatga tatgataaaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctcctcaga 1680
aaaataaaaga ggagg 1695

<210> 154

<211> 565

<212> PRT

<213> Thermatoga maritima

<400> 154

Met	Ile	Pro	Arg	Glu	Val	Ile	Glu	Glu	Ile	Lys	Glu	Lys	Val	Asp	Ile
1					5				10				15		

Val	Glu	Val	Ile	Ser	Glu	Tyr	Val	Asn	Leu	Thr	Arg	Val	Gly	Ser	Ser
						20			25				30		

Tyr	Arg	Ala	Leu	Cys	Pro	Phe	His	Ser	Glu	Thr	Asn	Pro	Ser	Phe	Tyr
							35				40			45	

Val	His	Pro	Gly	Leu	Lys	Ile	Tyr	His	Cys	Phe	Gly	Cys	Gly	Ala	Ser
					50			55				60			

Gly	Asp	Val	Ile	Lys	Phe	Leu	Gln	Glu	Met	Glu	Gly	Ile	Ser	Phe	Gln
					65			70				75			80

Glu	Ala	Leu	Glu	Arg	Leu	Ala	Lys	Arg	Ala	Gly	Ile	Asp	Leu	Ser	Leu
						85			90				95		

Tyr	Arg	Thr	Glu	Gly	Thr	Ser	Glu	Tyr	Gly	Lys	Tyr	Ile	Arg	Leu	Tyr
							100		105			110			

Glu	Glu	Thr	Trp	Lys	Arg	Tyr	Val	Lys	Glu	Leu	Glu	Lys	Ser	Lys	Glu
					115			120				125			

Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala
130 135 140

Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu
145 150 155 160

Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly
165 170 175

Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg
180 185 190

Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly
195 200 205

Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu
210 215 220

Thr Arg Tyr Phe Ser Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala
225 230 235 240

Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr
245 250 255

Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala
260 265 270

Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala
275 280 285

Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe
290 295 300

Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn
305 310 315 320

Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe
325 330 335

Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg
340 345 350

Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg
355 360 365

Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp
370 375 380

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
385 390 395 400

Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
405 410 415

Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
420 425 430

Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
435 440 445

Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
450 455 460

Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
465 470 475 480

Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
485 490 495

Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
500 505 510

Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
515 520 525

Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
530 535 540

Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
545 550 555 560

Lys Ile Lys Arg Arg
565

<210> 155
<211> 804
<212> DNA
<213> Thermus thermophilus

<400> 155
atggctctac acccggtca ccctggggca ataatgggc acgaggccgt tctcgccctc 60
cttccccgcc tcaccggcca gaccctgctc ttctccggcc ccgagggggt gggcgccgc 120
accgtggccc gctggtaacgc ctgggggctc aaccgcggct tccccccgccc ctccctgggg 180
gagcacccgg acgtcctcga ggtggggccc aaggccccggg acctccgggg ccggccgag 240

gtcggtggcaggaggctggccccccttggatgggtgcctagccaccccgggagcgg 300
gtgaagggtggccatcctgga ctcggcccac ctccctcaccg aggccgcgc caacgcctc 360
ctcaagctcc tggaggagcc cccttcctac gcccgcacg tcctcategc cccaagccgc 420
gccaccctcc tccccaccct gcctcccccgg gccacggagg tggcattgc ccccggtgccc 480
gaggaggccc tgccgcgcct cacccaggac ccggagctcc tccgctacgc cgccggggcc 540
ccggggccgc tccttagggc cttccaggac ccggagggtt accgggcccgc atggccagg 600
gcccggaaaggc tcctgaaaagc cccgcctcg gagcgcctcg ctttgctcg ggagctttg 660
gcccggaggagg aggggtcca cccctccac gccgtcctaa agcgcgggga gcacctcctt 720
gcccggggc gggcgcggga ggcctggag gggtaactgtga gccccgagct ggtcctcgcc 780
cgctggcct tagacttaga gaca 804

<210> 156

<211> 268

<212> PRT

<213> Thermus thermophilus

<400> 156

Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
1 5 10 15

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
20 25 30

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
35 40 45

Gly Leu Asn Arg Gly Phe Pro Pro Ser Leu Gly Glu His Pro Asp
50 55 60

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
65 70 75 80

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
85 90 95

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
100 105 110

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
115 120 125

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
130 135 140

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
145 150 155 160

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
165 170 175

Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu
180 185 190

Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro
195 200 205

Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu
210 215 220

Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu
225 230 235 240

Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu
245 250 255

Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr
260 265

<210> 157

<211> 729

<212> DNA

<213> Thermus thermophilus

<400> 157

atgttggacc tgagggaggt gggggaggcg gagtggagg ccctaaagcc cctttggaa 60
agcgtgcccgg agggcggtccc cgtccttcctc ctggacccta agccaagccc ctcccggcg 120
gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180
cggcacctgg aaaaccgggc caagcgctg gggctcaggg tcccggggcg ggtggcccg 240
tacctggcct ccctggaggg ggacctcgag gccctggagc gggagctggaa gaagcttgcc 300
ctcctctccc caccctcac cctggagaag gtggagaagg tggtggccct gaggcccccc 360
ctcacgggct ttgacctggt gcgcctcgat ctggagaagg accccaagga gcgcctcctg 420
cgccctaggcg gcctcaagga ggagggggag gagccctca ggctcctcg ggccctctcc 480
tggcagttcg ccctcctcgcc cccggccttc ttccctcctcc gggaaaaacc caggcccaag 540
gaggaggacc tcacggaga ggcctcaag gaggccctgg acgcctcat ggaggcggaa 600
gcgaagcgcc tcacggaga ggcctcaag gaggccctgg acgcctcat ggaggcggaa 660
aagagggcca agggggggaa agacccgtgg ctcgcctgg aggcggcggt ctcgcctc 720
gcgcgttga 729

<210> 158

<211> 292

<212> PRT

<213> Thermus thermophilus

<400> 158

Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
50 55 60

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
65 70 75 80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
85 90 95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
100 105 110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
115 120 125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
130 135 140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
145 150 155 160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
165 170 175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
180 185 190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
195 200 205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
210 215 220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
225 230 235 240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
245 250 255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275 280 285

Arg Leu Ala Arg
290

<210> 159
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159
gtgtgtcata tgagtaagga tttcgtccac cttcacc 37

<210> 160
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gtgtgtggat ccggggacta ctcggaagta aggg 34

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gtgtgtcata tggaaaccac aatattccag ttccag 36

<210> 162

<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 162
gtgtgtggat ccttatccac catgagaagt atttttcac 39

<210> 163
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 163
gtgtgtcata tggaaaaagt ttttttggaa aaaaactccaa g 41

<210> 164
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 164
gtgtgtggat ccttaatccg cctgaacggc taacg 35

<210> 165
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 165
gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g 41

<210> 166

<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 166
gtgtgtggat ccttaaaaaca gcctcgccc gctgga 36

<210> 167
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 167
gtgtgtcata tgcgcgttaa ggtggacagg gag 33

<210> 168
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 168
tgtgtctcga gtcatggcta caccctcatc ggcatt 35

<210> 169
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 169
gtgtgtcata tgctcaataa ggttttata ataggaagac ttacggg 47

<210> 170

<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170

gtgtggatcc taaaaaaggt atttcgtcct cttcatcgg

39

<210> 171
<211> 807
<212> DNA
<213> Thermus thermophilus

<400> 171

atggctcgag gcctgaaccg cgaaaaaccc tcggccacccg gcccggacatg 60
cgctacaccc cggcgccccct cgccatTTTg gacctgaccc tcggccggtaa ggacacctgctt 120
ctttccgata acgggggggg accggagggtg tcctggtaacc accggggtag 90 gctcttaggc 180
cgcccaggcgg agatgtgggg cgacacttgc gaccaaggc agctcgctt cgtggaggc 240
cgccctggagt accggccagtq qgaaaggaggg ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggacccctg gacgaccggg ggaagaagcg ggccggaggac agccggggcc 360
agcccaggct ccgcggccgc ctgaaccagg tcttcctcat gggcaacctg acccgggacc 420
cggaactccg ctacacccccc cagggcaccc cggtggcccg gctgggcctg gcggtgaacg 480
agcgccgcca gggggcgag gagcgcaccc acttcgtgga gggtcaggcc tggcgccacc 540
tggcgagtg ggccggccgag ctgaggaagg ggcacggcct ttctcgatc ggcaggttgg 600
tgaacgactc ctggaccagc tccagcggcg agcgcgcctt ccagaccgt gtggaggccc 660
tcaggctgga ggcggccacc cgtggacctg cccaggcccg cggAACAGGT 720
cccgcgaaat ccagacgggt ggggtggaca ttgacgaagg cttggaaagac ttccggccgg 780
aggaggattt gccgttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> Thermus thermophilus

<400> 172

Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15

Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30

Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45

Glu	Val	Ser	Trp	Tyr	His	Arg	Val	Arg	Leu	Leu	Gly	Arg	Gln	Ala	Glu
50					55				60						
Met	Trp	Gly	Asp	Leu	Leu	Asp	Gln	Gly	Gln	Leu	Val	Phe	Val	Glu	Gly
65				70					75				80		
Arg	Leu	Glu	Tyr	Arg	Gln	Trp	Glu	Arg	Glu	Gly	Glu	Lys	Arg	Ser	Glu
		85						90				95			
Leu	Gln	Ile	Arg	Ala	Asp	Phe	Leu	Asp	Pro	Leu	Asp	Asp	Arg	Gly	Lys
		100					105				110				
Lys	Arg	Ala	Glu	Asp	Ser	Arg	Gly	Gln	Pro	Arg	Leu	Arg	Ala	Ala	Leu
		115				120				125					
Asn	Gln	Val	Phe	Leu	Met	Gly	Asn	Leu	Thr	Arg	Asp	Pro	Glu	Leu	Arg
		130			135				140						
Tyr	Thr	Pro	Gln	Gly	Thr	Ala	Val	Ala	Arg	Leu	Gly	Leu	Ala	Val	Asn
		145			150			155				160			
Glu	Arg	Arg	Gln	Gly	Ala	Glu	Glu	Arg	Thr	His	Phe	Val	Glu	Val	Gln
		165				170				175					
Ala	Trp	Arg	Asp	Leu	Ala	Glu	Trp	Ala	Ala	Glu	Leu	Arg	Lys	Gly	Asp
		180				185				190					
Gly	Leu	Phe	Val	Ile	Gly	Arg	Leu	Val	Asn	Asp	Ser	Trp	Thr	Ser	Ser
		195			200				205						
Ser	Gly	Glu	Arg	Arg	Phe	Gln	Thr	Arg	Val	Glu	Ala	Leu	Arg	Leu	Glu
		210			215				220						
Arg	Pro	Thr	Arg	Gly	Pro	Ala	Gln	Ala	Cys	Pro	Gly	Arg	Arg	Asn	Arg
		225			230			235				240			
Ser	Arg	Glu	Val	Gln	Thr	Gly	Gly	Val	Asp	Ile	Asp	Glu	Gly	Leu	Glu
		245				250				255					
Asp	Phe	Pro	Pro	Glu	Glu	Asp	Leu	Pro	Phe						
		260				265									

<210> 173
<211> 992
<212> DNA
<213> *Bacillus stearothermophilus*

<400> 173

aattccgaca tttcaattga atcgtttatt ccgcttgaaa aagaaggcaa gttgctcggt 60
gatgtaaaaa gaccggggag catcgtaactg caggcgcgtt tttctctga aatcgtaaaa 120
aaactgccgc aacaaacggt gaaaatcgaa acggaagaca acttttgc gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaacgccc acgaatatcc gcgcctgccc 240
caaattgaag aagaaaacgt gttcaaattc ccggctgatt tattgaaaac cgtgattcgg 300
caaacggtgt tcgcccgtt tacatcgaa acgcgcacca tcttgcacagg tgtcaactgg 360
aaagttgaac atggcgagct tgtctgcaca gcgaccgaca gtcatcgctt agccatgcgc 420
aaagtaaaaa ttgagtcgga aaatgaagta tcataacaacg tcgtcatccc tgaaaaaagt 480
cttaatgagc tcagaaaaat ttggatgac ggcaaccacc cggtggacat cgcatgaca 540
gccaatcaag tgctattaa gcccggacac cttcttttctt tttcccgct gcttgcacggc 600
aactatccgg agacggcccc cttgattcca acagaaaagca aaacgaccat gatcgtaat 660
gcaaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaac 720
aacgttgtga aactgacgac gcttcctgga ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgcacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cggtgcggc gcttgcgttgc acagacattt 900
caaatcagct tcactggggc catgcggccg ttccctgttgc gcccgcattca accgattcga 960
tgcttcagct cattttgccc gtgagaacat at 992

<210> 174

<211> 334

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 174

Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
1 5 10 15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
20 25 30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
35 40 45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
50 55 60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
65 70 75 80

Pro Gln Ile Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
85 90 95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
100 105 110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu

115	120	125
Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys		
130	135	140
Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly		
145	150	160
Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His		
165	170	175
Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu		
180	185	190
His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr		
195	200	205
Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala		
210	215	220
Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu		
225	230	240
Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu		
245	250	255
Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu		
260	265	270
Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala		
275	280	285
Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln		
290	295	300
Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His		
305	310	320
Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr		
325	330	

<210> 175
<211> 492
<212> DNA
<213> *Bacillus stearothermophilus*

<400> 175

atgattaacc gcgtcatttt ggtcgccagg ttaacgagag atccggagtt gcgttacact 60
ccaagcggag tggctgttgc cacgtttacg ctcgcggtca accgtccgtt tacaaaatcg 120
cagggcgagc gggaaacgga ttttattcaa tgtgtcggtt ggcgcgcga ggcggaaaac 180
gtcgccaaact ttttggaaaaa ggggagcttg gctgggtcg atggccgact gcaaaccgc 240
agctatgaaa atcaagaagg tcggcgtgtg tacgtacgg aagtggtggc tgatagcgtc 300
caatttcttg agccgaaagg aacgagcagc cagcgggggg cgacagcagg cggctactat 360
ggggatccat tcccattcgg gcaagatcg aaccaccaat atccgaacga aaaagggttt 420
ggccgcatacg atgacgatcc ttgcggccat gacggccagc cgatcgatat ttctgtat 480
gatttgcgt tt 492

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
1 5 10 15

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
20 25 30

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
35 40 45

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
50 55 60

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
65 70 75 80

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
85 90 95

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
100 105 110

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
115 120 125

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
130 135 140

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
145 150 155 160

Asp Leu Pro Phe

<210> 177
<211> 1044
<212> DNA
<213> *Bacillus stearothermophilus*

<400> 177
atgcttggAAC gcgttatgggg aaacattgaa aaacggcgTT tttctccCT ttatttatta 60
tacggcaatg agccgtttt attaacggaa acgtatgagc gattggtaAA cgcaGcgCTT 120
ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaAA gccgatcgag 180
gcggcgCTT aggaggCCGA gacggtgCCG ttttcggcg agcggcgTGT catttcATC 240
aagcatccat attttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
ctggaggcgt acttgaaggc gccgtcgCCG ttttcgatcg tcgtctttt cgcGCCgtac 360
gagaagctt atgagcgaaa aaaaattacg aagctcgcca aagagcaaAG cgaagtCGTC 420
atcgccgccc cgctcgCCGA agcggagCTG cgtgcctggg tgccggcGCC catcgagAGC 480
caagggcgc aagcaagcga cgaggcgatt gatgtccTGT tgccggggc cgggacgcAG 540
ctttccgcct tggcgaatga aatcgataAA ttggccCTGT ttgcccggatc gggcggAAC 600
atcgaggcgg cggcggttga gcccgttgc gcccgcACGC cggaaAGAAA cgtatTTGT 660
cttgcgagc aagtggcgaa ggcgcacatt ccagcagcgt tgccgacgtt ttatgtatCTG 720
cttggaaaaaca atgaagagcc gatcaaaATT ttggcgTTGC tgccggCCA tttccgCTTG 780
ctttcgcaag tgaaatggct tgccctcTTA ggctacggac aggcgcaaAT tgctcgccg 840
ctcaaggTgc acccgTTCCG cgtcaagCTC gctcttgCTC aagcggcccG cttcgctgac 900
ggagagctt ctgaggcgat caacgagCTC gctgacgcccG attacgaAGT gaaaagcggg 960
gcggtcgatc gccgggtggc cgtttagctg cttctgatgc gctggggcgc cccggcggcg 1020
caagcggggc gccacggccg gcgg 1044

<210> 178
<211> 348
<212> PRT
<213> *Bacillus stearothermophilus*

<400> 178
Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
1 5 10 15

Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
20 25 30

Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
35 40 45

Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
50 55 60

Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

65	70	75	80
Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His			
85	90		95
Asp Leu Ala Lys Leu Glu Ala Tyr Leu Lys Ala Pro Ser Pro Phe Ser			
100	105		110
Ile Val Val Phe Phe Ala Pro Tyr Glu Lys Leu Asp Glu Arg Lys Lys			
115	120		125
Ile Thr Lys Leu Ala Lys Glu Gln Ser Glu Val Val Ile Ala Ala Pro			
130	135	140	
Leu Ala Glu Ala Glu Leu Arg Ala Trp Val Arg Arg Arg Ile Glu Ser			
145	150	155	160
Gln Gly Ala Gln Ala Ser Asp Glu Ala Ile Asp Val Leu Leu Arg Arg			
165	170		175
Ala Gly Thr Gln Leu Ser Ala Leu Ala Asn Glu Ile Asp Lys Leu Ala			
180	185		190
Leu Phe Ala Gly Ser Gly Gly Thr Ile Glu Ala Ala Val Glu Arg			
195	200		205
Leu Val Ala Arg Thr Pro Glu Glu Asn Val Phe Val Leu Val Glu Gln			
210	215		220
Val Ala Lys Arg Asp Ile Pro Ala Ala Leu Gln Thr Phe Tyr Asp Leu			
225	230		240
Leu Glu Asn Asn Glu Glu Pro Ile Lys Ile Leu Ala Leu Leu Ala Ala			
245	250		255
His Phe Arg Leu Leu Ser Gln Val Lys Trp Leu Ala Ser Leu Gly Tyr			
260	265		270
Gly Gln Ala Gln Ile Ala Ala Leu Lys Val His Pro Phe Arg Val			
275	280		285
Lys Leu Ala Leu Ala Gln Ala Ala Arg Phe Ala Asp Gly Glu Leu Ala			
290	295		300
Glu Ala Ile Asn Glu Leu Ala Asp Ala Asp Tyr Glu Val Lys Ser Gly			
305	310		320
Ala Val Asp Arg Arg Leu Ala Val Glu Leu Leu Met Arg Trp Gly			

325

330

335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
 340 345

<210> 179
 <211> 757
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 179
 atgcgtatggg aacagctagc gaaacgccag ccgggttgtgg cggaaaatgct gcaaaaggcc 60
 ttggaaaaag ggcggatttc tcatgcgtac ttgtttgagg ggcagcgccc gacgggcaaa 120
 aaagcggcca gtttgttggt ggcgaaacgt ttgtttgtc tgtccccat cgaggtttcc 180
 ccgtgtctag agtgcgcgcaa ctgcgcgcgc atcgactccg gcaaccaccc tgacgtccgg 240
 gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300
 ttctcgaaaaa cagcgtcga gtcggataaaa aaaatgtaca tcggttagaca cgccgatcaa 360
 atgacgacaa ggcgtccaa cagccttctg aaattttgg aagagccca tccggggacg 420
 gtggcggtat tgctgactga gcaataccac cgcctgctag ggacgatcggt ttcccgctgt 480
 caagtgcctt cgttccggcc gttgcccgcg gcagagctcg cccaggact tgtcgaggag 540
 cacgtgccgt tgccgttggc gctgttggtc gcccatttga caaacagctt cgaggaagca 600
 ctggcgcttg ccaaagatag ttgggttgcg gaggcgcgaa cattagtgtc acaatggtat 660
 gagatgctgg gcaagccgga gctgcagctt ttgttttca tccacgaccg cttgtttccg 720
 catttttgg aaagccatca gcttgacctt ggacttg 757

<210> 180
 <211> 252
 <212> PRT
 <213> *Bacillus stearothermophilus*

<400> 180
 Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
 1 5 10 15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
 20 25 30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Ala
 35 40 45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
 50 55 60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
 65 70 75 80

Val	Ile	Gly	Pro	Asp	Gly	Gly	Ser	Ile	Lys	Lys	Glu	Gln	Ile	Glu	Trp
			85						90					95	
Leu	Gln	Gln	Glu	Phe	Ser	Lys	Thr	Ala	Val	Glu	Ser	Asp	Lys	Lys	Met
			100						105				110		
Tyr	Ile	Val	Glu	His	Ala	Asp	Gln	Met	Thr	Thr	Ser	Ala	Ala	Asn	Ser
			115						120				125		
Leu	Leu	Lys	Phe	Leu	Glu	Glu	Pro	His	Pro	Gly	Thr	Val	Ala	Val	Leu
		130			135					140					
Leu	Thr	Glu	Gln	Tyr	His	Arg	Leu	Leu	Gly	Thr	Ile	Val	Ser	Arg	Cys
		145			150				155				160		
Gln	Val	Leu	Ser	Phe	Arg	Pro	Leu	Pro	Pro	Ala	Glu	Leu	Ala	Gln	Gly
			165						170				175		
Leu	Val	Glu	Glu	His	Val	Pro	Leu	Pro	Leu	Ala	Leu	Leu	Ala	Ala	His
		180					185				190				
Leu	Thr	Asn	Ser	Phe	Glu	Glu	Ala	Leu	Ala	Leu	Ala	Lys	Asp	Ser	Trp
		195					200			205					
Phe	Ala	Glu	Ala	Arg	Thr	Leu	Val	Leu	Gln	Trp	Tyr	Glu	Met	Leu	Gly
		210				215				220					
Lys	Pro	Glu	Leu	Gln	Leu	Leu	Phe	Phe	Ile	His	Asp	Arg	Leu	Phe	Pro
		225				230			235				240		
His	Phe	Leu	Glu	Ser	His	Gln	Leu	Asp	Leu	Gly	Leu				
			245				250								

<210> 181

<211> 1677

<212> DNA

<213> Bacillus stearothermophilus

<400> 181

```
gtggcatacc aagcgttata tcgcgtgttt cggccgcagc gctttgcgga catggtcggc 60
caagaacacg tgacccaagac gttgcaaagc gcccgtcttc aacataaaat atgcacgct 120
tacttatttt ccggcccgcg cggtacagga aaaacgagcg cagcggaaat tttcgccaag 180
gcggtaact gtgaacacaggc gccagcggcg gagccatgca atgagtgtcc agcttgccctc 240
ggcattacga atggaacggc tcccgtatgt ctggaaattt acgctgcttc caacaaccgc 300
gtcgatgaaa ttctgtatccgtgagaag gtgaaatttgc cggcaacgtc ggcccgctac 360
aaagtgtata tcatcgacga ggtgcataatgc ctgtcgatgc gtgcgtttaa cgcgctgttgc 420
aaaacgttgg aggagccgcc gaaacacgtc attttcattt tggccacgac cgagccgac 480
```

aaaattccgg cgacgatcat ttcccgtgc caacggttcg atttcgtccg catcccgctt 540
caggcgtatcg tttcacggct aaagtacgtc gcaagcgccc aaggtgtcga ggcgtcagat 600
gaggcattgt ccgcgcattcg cctgtgtca gacggggggta tgccgtatgc gtcagcttg 660
cttgcgtcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg catcatatgc cgccttatcg agcttcatcg aagccatcca ccgaaagat 780
acagcggcgg ttcttcagca ctggaaacg atgatggcgc aaggaaaga tccgcacgt 840
ttgggtgaag acttgatcccgtt gtttattgc tgtacaac cgctccctat 900
gtggaggag cgattcaaataat tgctgtcggtt gacgaagcgt tcacttcact gtcggaaatg 960
atccgggtt ccaattata cgaggccatc gagttgtga acaaaagcca gcaagagatg 1020
aagtggacaa accaccccgccg cttctgttg gaagtggcgc ttgtgaaact ttgcacatcca 1080
tcagccgcgg ccccggtcgatc gtcggcttcc gagttggaaac cggtgataaa gcggattgaa 1140
acgctggagg cggaatttgcg ggcctgtaaag gaacaaccgc ctggccctcc gtcgaccgc 1200
gcgccgggtga aaaaactgtc caaaccgatg aaaacggggg gatataaagc cccgggtggc 1260
cgcatatcg agctgtgaa acaggcgacg catgaagatt tagcttggt gaaaggatgc 1320
tggcggatg tgctcgacac gttgaaacgg cagcataaag tgtcgacgc tgccttgctg 1380
caagagagcg agccgggtgc agcgagcgc tcagcggtt tattaaattt caaatacga 1440
atccactgca aaatggcgac cgatcccaca agttcggtca aagaaaacgt cgaagcgatt 1500
ttgttgagc tgacaaaccg cccgtttgaa atggtagcca ttccggaggg agaatgggg 1560
aaaataagag aagagttcat ccgcaataag gacgccatgg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggctgttt ggcgaagagc tgatcgaaat taaagaa 1677

<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

Val	Ala	Tyr	Gln	Ala	Leu	Tyr	Arg	Val	Phe	Arg	Pro	Gln	Arg	Phe	Ala
1								10						15	

Asp	Met	Val	Gly	Gln	Glu	His	Val	Thr	Lys	Thr	Leu	Gln	Ser	Ala	Leu
									25					30	

Leu	Gln	His	Lys	Ile	Ser	His	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly
									35				40		45

Thr	Gly	Lys	Thr	Ser	Ala	Ala	Lys	Ile	Phe	Ala	Lys	Ala	Val	Asn	Cys
								50					55		60

Glu	Gln	Ala	Pro	Ala	Ala	Glu	Pro	Cys	Asn	Glu	Cys	Pro	Ala	Cys	Leu
								65					70		80

Gly	Ile	Thr	Asn	Gly	Thr	Val	Pro	Asp	Val	Leu	Glu	Ile	Asp	Ala	Ala
								85					90		95

Ser	Asn	Asn	Arg	Val	Asp	Glu	Ile	Arg	Asp	Ile	Arg	Glu	Lys	Val	Lys
								100					105		110

Phe Ala Pro Thr Ser Ala Arg Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Lys His Val Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145 150 155 160

Lys Ile Pro Ala Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Arg
165 170 175

Arg Ile Pro Leu Gln Ala Ile Val Ser Arg Leu Lys Tyr Val Ala Ser
180 185 190

Ala Gln Gly Val Glu Ala Ser Asp Glu Ala Leu Ser Ala Ile Ala Arg
195 200 205

Ala Ala Asp Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala
210 215 220

Ile Ser Phe Ser Asp Gly Lys Leu Arg Leu Asp Asp Val Leu Ala Met
225 230 235 240

Thr Gly Ala Ala Ser Phe Ala Ala Leu Ser Ser Phe Ile Glu Ala Ile
245 250 255

His Arg Lys Asp Thr Ala Ala Val Leu Gln His Leu Glu Thr Met Met
260 265 270

Ala Gln Gly Lys Asp Pro His Arg Leu Val Glu Asp Leu Ile Leu Tyr
275 280 285

Tyr Arg Asp Leu Leu Tyr Lys Thr Ala Pro Tyr Val Glu Gly Ala
290 295 300

Ile Gln Ile Ala Val Val Asp Glu Ala Phe Thr Ser Leu Ser Glu Met
305 310 315 320

Ile Pro Val Ser Asn Leu Tyr Glu Ala Ile Glu Leu Leu Asn Lys Ser
325 330 335

Gln Gln Glu Met Lys Trp Thr Asn His Pro Arg Leu Leu Leu Glu Val
340 345 350

Ala Leu Val Lys Leu Cys His Pro Ser Ala Ala Ala Pro Ser Leu Ser
355 360 365

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380

 Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400

 Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415

 Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430

 Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445

 Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460

 Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480

 Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495

 Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510

 Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525

 Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540

 Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183

<211> 4301

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 183

atggtgacaa aagagcaaaa agagcggttt ctcatcctgc ttgagcagct gaagatgacg 60
 tcggacgaat ggtatgccca ttttctgttag gcagccattc gcaaagtctgt gatcgataaa 120
 gaggagaaaa gctggcattt ttatttctag ttccgacaacg tgctgccggt tcatgtatac 180
 aaaacgtttg ccgatcggtt gcagacggcg ttccggccata tcgcccgggt ccggccataacg 240

atggaggctcg aagcgcgcg cgtaactgag gcggatgtgc aggcgtattt gcccgtttgc 300
cttgcgcgac tgcagaagg catgtcgccg cttgtcgatt ggctcagccg gcagacgcct 360
gagctgaaag gaaacaagot gcttgcgtt gcccgcattg aagcggaaagc gctggcgatc 420
aaacggcggt tcgccccaaa aatcgctgat gtgtacgctt cgtttgggtt tccccccctt 480
cagcttgacg tcagcgtcga gccgtccaag caagaaatgg aacagttttt ggcgcaaaaa 540
cagcaagagg acgaagagcg agcgcttgct gtactgaccg atttagcgag ggaagaagaa 600
aaggccgcgt ctgcgcgcgc gtccggtccg cttgtcatcg gctatccgat ccgcgacgag 660
gagccggtgc ggcggcttga aacgatcgac gaagaagagc ggcgcgtcgt tgtgcaaggc 720
tatgtatTTT acgcccgaagt gagcgaatta aaaagcggcc gcacgctgtt gaccatgaaa 780
atcacagatt acacgaactc gatTTtagtc aaaatgttct cgcgacgacaa agaggacgcc 840
gagcttatga gccgcgtcaa aaaaggcatg tgggtgaaag tgccgcggcag cgtcaaaac 900
gatacgttcg tccgtgattt ggtcatcatc gccaacgatt tgaacgaaaat cgccgcaaaac 960
gaacggcaag atacggcgcc ggaagggaa aagagggtcg agctccattt gcataccccc 1020
atgagccaaa tggacgcgtt cacccgggtg acaaaaactca ttgagcaagc gaaaaaatgg 1080
gggcattccgg cgatcgccgt caccgaccat gccgttggc agtgcgttcc ggaggcctac 1140
agcgcgcgca aaaaacacgg catgaaggc atttacggcc ttgaggcgaa catcgac 1200
gatggcgtgc cgatcgcccta caatgagacg caccgcgtc tttcgagga aacgtacgtc 1260
gtctttgacg tcgagacgac gggcctgtcg gctgtgtaca atacgatcat tgagctggcg 1320
gcggtaaaag tgaagacgg cgagatcatc gaccgattca tgctgttgc caaccctgga 1380
catccgttgc cggtgacaac gatggagctg actggatca ccgtatgagat ggtgaaagac 1440
gccccgaagc cgacgaggt gctagccgt tttgttact gggccggcga tgcacgcctt 1500
gttgcacaca acgcacgct tgacatcggt tttttaaacg cgggcctcgc tcgcacgggg 1560
cgccggcaaaa tcgcgaatcc agtcatcgat acgctcgagc tggcccggtt ttataccgg 1620
gatttggaaa accatcggtt caatacattt tgcaaaaaat ttgacattga attgacgcag 1680
catcaccgcg ccatctacga cgcggaggcg accgggcatt tgcttatgcg gctgttgaag 1740
gaagcgaag agcgcggcat actgtttcat gacgaattaa acagccgcac gcacagcgaa 1800
gcgtccatc ggcttgcgcg cccgttccat gtacgcgtgt tggcgcaaaa cgagactgga 1860
ttgaaaaatt tttcaagct tttgtcattt tcgcacattt aatattttca ccgtgtgccc 1920
cgcatccgcg gctccgtgt cgtcaagcac cgcgcacggcc tgcttgcgg ctcggcgtc 1980
gacaaaggag agctgtttga caacttgcattt caaaaaggcgc cggaagaagat cgaagacatc 2040
gcccgtttt acgattttct tgaagtgcattt ccggcggacg tgcacggcc gctcatcgag 2100
atggattatg tgaagacga agagatgatc aaaaacatca tccgcacatc cgtcgcctt 2160
ggtgagaagc ttgacatccc gttgtcgcc actggcaacg tccattactt gaaccaggaa 2220
gataaaattt accggaaaat cttaatccat tcgcaaggcg gggcgaatcc gctcaaccgc 2280
catgaactgc cgatgtata tttccgtacg acgaatggaa tgcttgactt cttctcgtt 2340
ttagggccgg aaaaagcgaa ggaaatcgac gttgacaaca cgcaaaaaat cgcttcgtta 2400
atcgccatg tcaagccgat caaagatgag ctgtatacg cgcgcatttga agggccggac 2460
gaggaaatca ggaaatgag ctaccggcg gcgaaaggaaa ttacggcga cccgttgccc 2520
aaacttgggg aagagcggct tgagaaggag ctaaaaagca tcacggccca tggcttgc 2580
gtcattttt tgcacatcgat caagttgtt aaaaatcgatc tgcacggatc ctacccgtt 2640
gggtcgccgcg gatcggtcggt ctcgtcgat tgcgcacgc tgacggaaat caccgaggc 2700
aatccgcgtc cgccgcattt cgtttgcgg aactgcacgc attcgagtt cttaacgc 2760
ggttcagtcg gtcagggtt tgatttgcg gataaaaaact gcccgcgtt gggacgaaa 2820
tacaagaaag acgggcacga catcccgat tttttttttt gagacgtttc tcggctttaa agggcaca 2880
gtgccgata tcgacttgcgaa cttttccggc gaataccagc cgcgcgcggca caactatacg 2940
aaagtgcgtt ttggcgaaga caacgtctac cgcgcggga cgattggcact ggtcgctgac 3000
aaaacggcgatc acggattttt gaaacgtat gcgacgcacc ataacttaga gtcgcgcggc 3060
gcggaaatcg acggctcgcc gtcggctgca ccgggggtgaa gcggacgcacc gggcagcatc 3120

cggcgccat catcgctgc tcggattata tggaaattta cgattttacg ccgattcaat 3180
 atccggccga tgacacgtcc tctgaatggc ggacgaccga tttcgacttc cattcgatcc 3240
 acgacaattt gttgaagctc gatattctcg ggcacgacga tccgacggtc attcgcatgc 3300
 tgcaagattt aagcgccatc gatccgaaaa cgatccgac cgacgaccgg gatgtgtatgg 3360
 gcatttttag cagcaccgag cccgcttggcg ttacgcccga gcaaatacg tgcaatgtcg 3420
 gcacgatcggt cattccggag tttggcacgc gcttcgttcg gcaaatacg gaagagacaa 3480
 ggccaaaaac gtttccgaa ctcgtcaaaa ttccggctt gtcgcacggc accgatgtgt 3540
 ggctcgccaa cgccaaagag ctcattcaaa acggcacgtg tacgttatcg gaagtcatcg 3600
 gctgccgcga cgacattatg gtctatttgat ttaccgcgg gctcgagccg tcgctcgctt 3660
 ttaaaatcat ggaatccgtg cgccaaaggaa aaggcttaac gccggagttt gaagcagaaa 3720
 tgcgcaaaaca tgacgtgccc gagtggtaca tcgattcatg caaaaaaaaaa aagtacatgt 3780
 tccccaaagc gcacgcccgc gcctacgtgt taatggcggt gcgcacatcgcc tactttaagg 3840
 tgcacccatcc gctttgtat tacgcgtcg actttacggt gcggggcggag gactttgacc 3900
 ttgacgcccattt gatcaaaggaa tcacccgcca ttgcgaagcg gattgagaa atcaacgcca 3960
 aaggcattca ggcgacggcg aaagaaaaaa gcttgctcac ggttcttgag gtggccttag 4020
 agatgtgcga ggcgacggcg ttccctttttt atatcgattt gtaccgcgtc cagggcgtcg 4080
 aattcgtcat tgacggcaat tctctcattt cggccatttccg gggcttggga 4140
 cgaacgtggc gcaggcgatc gtgcgcgcgg gcgagggagg cgagtttttgcg tcaaggagg 4200
 atttgcaaca ggcgcccggaaa ttgtcgaaaaa cgctgctcgatgtatctagaa agccgcggct 4260
 gccttgactc gcttccagac cataaccagc tgtcgctgtt t 4301

<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

Met	Val	Thr	Lys	Glu	Gln	Lys	Glu	Arg	Phe	Leu	Ile	Leu	Leu	Glu	Gln
1				5					10					15	

Leu	Lys	Met	Thr	Ser	Asp	Glu	Trp	Met	Pro	His	Phe	Arg	Glu	Ala	Ala
								20			25			30	

Ile	Arg	Lys	Val	Val	Ile	Asp	Lys	Glu	Glu	Lys	Ser	Trp	His	Phe	Tyr
								35				40		45	

Phe	Gln	Phe	Asp	Asn	Val	Leu	Pro	Val	His	Val	Tyr	Lys	Thr	Phe	Ala
								50			55		60		

Asp	Arg	Leu	Gln	Thr	Ala	Phe	Arg	His	Ile	Ala	Ala	Val	Arg	His	Thr
								65			70		75		80

Met	Glu	Val	Glu	Ala	Pro	Arg	Val	Thr	Glu	Ala	Asp	Val	Gln	Ala	Tyr
								85			90			95	

Trp	Pro	Leu	Cys	Leu	Ala	Glu	Leu	Gln	Glu	Gly	Met	Ser	Pro	Leu	Val
								100			105		:	110	

Asp Trp Leu Ser Arg Gln Thr Pro Glu Leu Lys Gly Asn Lys Leu Leu
115 120 125

Val Val Ala Arg His Glu Ala Glu Ala Leu Ala Ile Lys Arg Arg Phe
130 135 140

Ala Lys Lys Ile Ala Asp Val Tyr Ala Ser Phe Gly Phe Pro Pro Leu
145 150 155 160

Gln Leu Asp Val Ser Val Glu Pro Ser Lys Gln Glu Met Glu Gln Phe
165 170 175

Leu Ala Gln Lys Gln Glu Asp Glu Glu Arg Ala Leu Ala Val Leu
180 185 190

Thr Asp Leu Ala Arg Glu Glu Lys Ala Ala Ser Ala Pro Pro Ser
195 200 205

Gly Pro Leu Val Ile Gly Tyr Pro Ile Arg Asp Glu Glu Pro Val Arg
210 215 220

Arg Leu Glu Thr Ile Val Glu Glu Glu Arg Arg Val Val Val Gln Gly
225 230 235 240

Tyr Val Phe Asp Ala Glu Val Ser Glu Leu Lys Ser Gly Arg Thr Leu
245 250 255

Leu Thr Met Lys Ile Thr Asp Tyr Thr Asn Ser Ile Leu Val Lys Met
260 265 270

Phe Ser Arg Asp Lys Glu Asp Ala Glu Leu Met Ser Gly Val Lys Lys
275 280 285

Gly Met Trp Val Lys Val Arg Gly Ser Val Gln Asn Asp Thr Phe Val
290 295 300

Arg Asp Leu Val Ile Ile Ala Asn Asp Leu Asn Glu Ile Ala Ala Asn
305 310 315 320

Glu Arg Gln Asp Thr Ala Pro Glu Gly Glu Lys Arg Val Glu Leu His
325 330 335

Leu His Thr Pro Met Ser Gln Met Asp Ala Val Thr Ser Val Thr Lys
340 345 350

Leu Ile Glu Gln Ala Lys Lys Trp Gly His Pro Ala Ile Ala Val Thr
355 360 365

Asp His Ala Val Val Gln Ser Phe Pro Glu Ala Tyr Ser Ala Ala Lys
370 375 380

Lys His Gly Met Lys Val Ile Tyr Gly Leu Glu Ala Asn Ile Val Asp
385 390 395 400

Asp Gly Val Pro Ile Ala Tyr Asn Glu Thr His Arg Arg Leu Ser Glu
405 410 415

Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val
420 425 430

Tyr Asn Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Asp Gly Glu
435 440 445

Ile Ile Asp Arg Phe Met Ser Phe Ala Asn Pro Gly His Pro Leu Ser
450 455 460

Val Thr Thr Met Glu Leu Thr Gly Ile Thr Asp Glu Met Val Lys Asp
465 470 475 480

Ala Pro Lys Pro Asp Glu Val Leu Ala Arg Phe Val Asp Trp Ala Gly
485 490 495

Asp Ala Thr Leu Val Ala His Asn Ala Ser Phe Asp Ile Gly Phe Leu
500 505 510

Asn Ala Gly Leu Ala Arg Met Gly Arg Gly Lys Ile Ala Asn Pro Val
515 520 525

Ile Asp Thr Leu Glu Leu Ala Arg Phe Leu Tyr Pro Asp Leu Lys Asn
530 535 540

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
545 550 555 560

His His Arg Ala Ile Tyr Asp Ala Glu Ala Thr Gly His Leu Leu Met
565 570 575

Arg Leu Leu Lys Glu Ala Glu Glu Arg Gly Ile Leu Phe His Asp Glu
580 585 590

Leu Asn Ser Arg Thr His Ser Glu Ala Ser Tyr Arg Leu Ala Arg Pro
595 600 605

Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu
610 615 620

Phe Lys Leu Val Ser Leu Ser His Ile Gln Tyr Phe His Arg Val Pro
625 630 635 640

Arg Ile Pro Arg Ser Val Leu Val Lys His Arg Asp Gly Leu Leu Val
645 650 655

Gly Ser Gly Cys Asp Lys Gly Glu Leu Phe Asp Asn Leu Ile Gln Lys
660 665 670

Ala Pro Glu Glu Val Glu Asp Ile Ala Arg Phe Tyr Asp Phe Leu Glu
675 680 685

Val His Pro Pro Asp Val Tyr Lys Pro Leu Ile Glu Met Asp Tyr Val
690 695 700

Lys Asp Glu Glu Met Ile Lys Asn Ile Ile Arg Ser Ile Val Ala Leu
705 710 715 720

Gly Glu Lys Leu Asp Ile Pro Val Val Ala Thr Gly Asn Val His Tyr
725 730 735

Leu Asn Pro Glu Asp Lys Ile Tyr Arg Lys Ile Leu Ile His Ser Gln
740 745 750

Gly Gly Ala Asn Pro Leu Asn Arg His Glu Leu Pro Asp Val Tyr Phe
755 760 765

Arg Thr Thr Asn Glu Met Leu Asp Cys Phe Ser Phe Leu Gly Pro Glu
770 775 780

Lys Ala Lys Glu Ile Val Val Asp Asn Thr Gln Lys Ile Ala Ser Leu
785 790 795 800

Ile Gly Asp Val Lys Pro Ile Lys Asp Glu Leu Tyr Thr Pro Arg Ile
805 810 815

Glu Gly Ala Asp Glu Glu Ile Arg Glu Met Ser Tyr Arg Arg Ala Lys
820 825 830

Glu Ile Tyr Gly Asp Pro Leu Pro Lys Leu Val Glu Glu Arg Leu Glu
835 840 845

Lys Glu Leu Lys Ser Ile Ile Gly His Gly Phe Ala Val Ile Tyr Leu
850 855 860

Ile Ser His Lys Leu Val Lys Lys Ser Leu Asp Asp Gly Tyr Leu Val
865 870 875 880

Gly Ser Arg Gly Ser Val Gly Ser Ser Phe Val Ala Thr Met Thr Glu
885 890 895

Ile Thr Glu Val Asn Pro Leu Pro Pro His Tyr Val Cys Pro Asn Cys
900 905 910

Lys His Ser Glu Phe Phe Asn Asp Gly Ser Val Gly Ser Gly Phe Asp
915 920 925

Leu Pro Asp Lys Asn Cys Pro Arg Cys Gly Thr Lys Tyr Lys Lys Asp
930 935 940

Gly His Asp Ile Pro Phe Glu Thr Phe Leu Gly Phe Lys Gly Asp Lys
945 950 955 960

Val Pro Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Pro Arg Ala
965 970 975

His Asn Tyr Thr Lys Val Leu Phe Gly Glu Asp Asn Val Tyr Arg Ala
980 985 990

Gly Thr Ile Gly Thr Val Ala Asp Lys Thr Ala Tyr Gly Phe Val Lys
995 1000 1005

Ala Tyr Ala Ser Asp His Asn Leu Glu Leu Arg Gly Ala Glu Ile Asp
1010 1015 1020

Leu Ala Ala Gly Cys Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro
1025 1030 1035 1040

Gly Gly Ile Ile Val Val Pro Asp Tyr Met Glu Ile Tyr Asp Phe Thr
1045 1050 1055

Pro Ile Gln Tyr Pro Ala Asp Asp Thr Ser Ser Glu Trp Arg Thr Thr
1060 1065 1070

His Phe Asp Phe His Ser Ile His Asp Asn Leu Leu Lys Leu Asp Ile
1075 1080 1085

Leu Gly His Asp Asp Pro Thr Val Ile Arg Met Leu Gln Asp Leu Ser
1090 1095 1100

Gly Ile Asp Pro Lys Thr Ile Pro Thr Asp Asp Pro Asp Val Met Gly
1105 1110 1115 1120

Ile Phe Ser Ser Thr Glu Pro Leu Gly Val Thr Pro Glu Gln Ile Met
1125 1130 1135

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val
1140 1145 1150

Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val
1155 1160 1165

Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala
1170 1175 1180

Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly
1185 1190 1195 1200

Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro
1205 1210 1215

Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu
1220 1225 1230

Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp
1235 1240 1245

Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His
1250 1255 1260

Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val
1265 1270 1275 1280

His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu
1285 1290 1295

Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys
1300 1305 1310

Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu
1315 1320 1325

Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg
1330 1335 1340

Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu
1345 1350 1355 1360

Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro
1365 1370 1375

Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu
1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe
1425 1430

<210> 185

<211> 199

<212> PRT

<213> Thermus thermophilus

<400> 185

Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
1 5 10 15

Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser
20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
65 70 75 80

Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
85 90 95

Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
100 105 110

Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
115 120 125

Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
130 135 140

Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
145 150 155 160

Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys

165

170

175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
180 185 190

Ala Gly Gln Pro Arg Val Asp
195

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

gcccaagtacc tcgcctccct cgagggg

27

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

ggcccccatttg gccttctcgg cctccat

27

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

agactcgagg ccctggaggcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60
ctggagaagg tggagaagggt ggtggccctg aggccccccc tcacgggctt tgacctggtg 120
cgctccgtcc tggagaagga ccccaaggag gccctctgc gcctcaggcg cctcagggag 180
gagggggagg agcccctcag gtcctcggg gccctctcct ggcagttcgc ctcctcgcc 240
cgggccttct tcctcctccg gaaaaacccc aggcccaagg aggaggacct cgcccgctc 300
gaggcccacc cctacgcccgc caagaaggcc a 331

<210> 189

160

<211> 110

<212> PRT

<213> Thermus thermophilus

<400> 189

Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
1 5 10 15

Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
20 25 30

Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
35 40 45

Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
50 55 60

Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
65 70 75 80

Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
85 90 95

Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
100 105 110

<210> 190

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 190

gtggtgtcta gacatcataa cggttctggc a

31

<210> 191

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 191

gaggggccacc actttctcca ccttctc

27

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 192
ctccgtcctg gagaaggacc ccaag

25

<210> 193
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<221> primer_bind
<222> (15)
<223> S at position 15 can be either C or G

<220>
<221> primer_bind
<222> (27)
<223> S at position 27 can be either C or G

<400> 193
cgcgattca acgcscctc caagacsc

29

<210> 194
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 194
gacacttaac atatggtcat cgccattcacc g

31

<210> 195
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 195
gtgtgtgaat tcgggtcaac gggcgaggcg gaggacg

38

<210> 196
<211> 10
<212> PRT
<213> Deinococcus radiodurans

<400> 196
Val Ile Leu Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 197
<211> 10
<212> PRT
<213> Methanococcus jannaschii

<400> 197
Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 198
<211> 10
<212> PRT
<213> Thermotoga maritima

<400> 198
Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
1 5 10

<210> 199
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 199
ctgggtgaacc cgggctccgt gggccagc

28

<210> 200
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 200
Leu Leu Val Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 201
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 201
ctcgaggagc ttgaggaggg tggc 27

<210> 202
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 202
Ala Asn Thr Leu Leu Lys Leu Leu Glu
1 5

<210> 203
<211> 32
<212> PRT

<213> Deinococcus radiodurans

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly
20 25 30

<210> 204

<211> 32

<212> PRT

<213> Caenorhabditis elegans

<400> 204

Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly
20 25 30

<210> 205

<211> 32

<212> PRT

<213> Pseudomonas aeruginosa

<400> 205

Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly
20 25 30

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggccacc tcctcaccga 30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr

1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtgggccg cgtggagctc cac 33

<210> 210
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 210
Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
1 5 10

<210> 211
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 211
ggctttccca tatggctcta cacccggctc ac 32

<210> 212
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 212
gcgtggatcc acggtcatgt ctctaagtc 29